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QY	1988	gtctcgtcgctcagaagaagccttgtgagacggaggaagcggcagaagcggcagcgctg	2047
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Oy	2228	acaatgatttccttccctaactlbaacaccataaaacacacacacacacacagtgg	2287
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Oy	2288	gatagcctggaacatgtcagcatgttaagaataaaggsgaatattatgaataagta	2339
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DEFINITION	HDMCAPLA	2240 bp	mRNA PRI 12-JUN-1995
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SOURCE	Cyto d sapiens fetus brain CDNA to mRNA.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
AUTHORS	Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 2240)		
JOURNAL	Sato,T., Irie,S. and Reed,J.C.		
MEDLINE	A novel member of the TRAF family of putative signal transducing		
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SOURCE	FEBs Lett. 358 (2), 113-118 (1995)		
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Best Local Similarity	96.3%;	Pred. No. 0;	
Matches 2185; Conservative	0; Mismatches	4; Indels	80; Gaps
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OY	136	acctggcccccgggcccct-gctccctactcttccaaagatccggtgtcccgacgaagaga	194
Db	61	ACCTGGCTCTTG6CTCCTGGCTCCCTTACTCTTTAAAGATCGCTGTCTGACGAAGAGAA	120
OY	195	actcctcttccctaanaatlygatcagtaaaagaatlygactccctcgggcgctgtcagac	254
Db	121	ACTCCTCTTCTTCTAAATAGAGAGTGGATTAATAAGATGAGATCTCTGTGGCGCTGTGAGAC	180
OY	235	taaccgcgcgtctaaagctgtcacactgtacgcgagtgctgtggagcgcaattgttccctga	314
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OY	315	acaaggaagtgtacaaggaanaagttgtfagaagacggtfagaagaaagtataaagtgtfaga	374
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OY	375	gtgccaccttggctgtgtgtgcaccccgaaagcagaccagttgtgggcacgcgtcttcgagag	434
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OY	435	ctgcaatggcgccctgtcgtagcttccaaagtcceaaatlytagcgtgttcaagagagcat	494
Db	361	CTGCATGTGCGCGCCCTGCTGACACTTTTCAATCCAAATGTACAGCGTGTCAAGAGAGCAT	420
OY	495	cgtaaagaataggtgtttaaggttaattgtctcaagagaagaaattcgtgccttcaagt	554
Db	421	CGTTAAATATAGGCTGTTTAAAGTAATCTGTCAAAAGAAATTCGTGACTTCATAGAT	480
OY	555	ctatgtctggaattaaagcagaagattgtgcagaagcagtaatactgtggagcat---ctgt	611
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OY	732	caaatgcagccactgtcagaagatctcagatgtcgtgcgtcagaaacaacgaagaacac	791
Db	661	CACATGCAAGCCACTGTGCAAGATCATAGTCTTCGATGATGTGCCCTGTCAAAACACGAACAC	720
OY	792	cgaatgtccctgtcgtgtgtgtgtgtcgtccctcaaaagtgcagcgtccagaactctctgag	851
Db	721	CGAGTGTCCCTGCGTGTGGTGTCTCTCCCTCAAAATGCAGGCTCCAGACTCTCTGAG	780
OY	852	gagcgaagtgtgcacactgtctagagtggttcaatgtcccccagaacactgttagtttaa	911
Db	781	GAGCG-----	785
OY	912	gcgctatgtcgtcgttttcaaggagcaaacacagcagatcaaggtccacgaagccagctc	971
Db	786	-----AGGGGCAAAACACAGCAGATTAAGGCCACACAGGCCACGACTC	825
OY	972	cgcgcgtgcagcagtlcaaacctgtctbaagagtggaagcaactcgtctcgaaaagaaagtttc	1031
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Db	1066	GGAGATCCGGATCTCTCCGCGAGAACTGGGAGAGACGACACACTGAAAGCGAGCTGTGA	11255
QY	1272	gtccctccagaacccgctgtgacccgagctgbyagacgtgtgacaagagcgcgcgggcaagtgc	13313
Db	1126	GTCCCTCCAGAACCGCGGTGACCGAGCTGGAGAGACGTGGACAAAGACGCGCGGCAAGTGGC	11855
QY	1332	tcggaaacaaagccctgtctgtgagtcceagctbagccggcatgacscagatgtctgagtgctga	13911
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QY	1392	cgaaatccggcccttagccgaactggaactggagcttcggagctccggagctggagccgcaagrtaa	14511
Db	1246	CGACATCCGCGCTTACCCGACACTGGAGCTGCGCTTCCAGGTCCTGGAGACCGCGAGCTTACAA	13055
QY	1452	tggagtgctcaactctggaagattcgcgactacaagcgcgcggaaagcagagagccgtcaatggtg	15111
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[illegible]

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Db	245	cgcctcagactaacccgcgcctaagctcgcacactgcagccgcagctctggaagccagttt	304		
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Db	305	ttgtccctgatacaagaagagttacaagaagaagtttgttgaagccgttggagagcaagtaca	364		
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DEFINITION Mus musculus CD40 receptor associated factor 1 (CRAF1) mRNA,
complete cds.
ACCESSION U21050
VERSION U21050.1 GI:719292
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE Cheng, G., Cleary, A.M., Ye, Z.S., Hong, D.I., Lederman, S. and
Baltimore, D.
INVOLVEMENT OF CRAF1, A RELATIVE OF TRAF, IN CD40 SIGNALING
JOURNAL Science 267 (5203), 1494-1498 (1995)
MEDLINE 95184010
REFERENCE 2 (bases 1 to 2359)
AUTHORS Cheng, G.
TITLE Direct Submission
JOURNAL Submitted (14-FEB-1995) Genhong Cheng, Biology, Massachusetts
Institute of Technology, 77 Massachusetts Avenue, Cambridge, MA
02139, USA

FEATURES
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	Oy	1442	ccagactcaaatgatgagtgctcatctcttgaaagattcgcgactacaacgcgcggaacgagagg	1501
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	Oy	1502	ccgtcatgggggaagacctctccctttaagccaagctttctaactgtaacttggct	1561
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REFERENCE 2 (bases 1 to 2222)
AUTHORS Nakano,H.
JOURNAL Unpublished (1996)
REFERENCE 3 (sites)
AUTHORS Nakano,H., Oshima,H., Chung,W., Williams-Abbott,L., Ware,C.F.,
Yagita,H. and Okumura,K.
TITLE TRAF5, an activator of NF-kappaB and putative signal transducer for
the lymphotoxin-beta receptor
JOURNAL J. Biol. Chem. 271 (25), 14661-14664 (1996)
MEDLINE 96278943
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QY	1878	agcatagtggatcattcgcgactctgcccgaatc	1909
Db	1963	AGTGCGCGTGGATTTAAGTGAAGTGGAGAGC	1994
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DEFINITION	Homo sapiens TNF receptor associated factor 5 mRNA, partial cds.		
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VERSION	U69108.1	GI:2138179	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	1 (bases 1 to 2738) Nakano, H., Shindo, M., Yamada, K., Yoshida, M.C., Santee, S.M., Ware, C.F., Jenkins, N.A., Gilbert, D.J., Yagita, H., Copeland, N.G. and Okumura, K.		
TITLE	Human TNF receptor-associated factor 5 (TRAF5): cDNA cloning, expression and assignment of the TRAF5 gene to chromosome 1q32		
JOURNAL	Genomics 42 (1), 26-32 (1997)		
REFERENCE	2 (bases 1 to 2738) Nakano, H., Shindo, M., Yagita, H. and Okumura, K.		
AUTHORS	Direct Submission		
JOURNAL	Submitted (02-SEP-1996) Department of Immunology, Juntendo University School of Medicine, 2-1-1 Hongo, Bunkyo-ku, Tokyo 113, Japan		
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CDS			
BASE COUNT	842 a 518 c 604 g 774 t		
ORIGIN			
Query Match	13.5%; Score 315.4; DB 11; Length 2738;		
Best Local Similarity	53.3%; Pred. No. 1.8e-59;		
Matches 854; Conservative	0; Mismatches 721; Indels 26; Gaps 8.		
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Db	38	AGTACACAGTTGTGGAGCGGTTGGAAGAGCGCTACAATGTCCTTGCCACTCGGTGC	97
QY	389	tgtgagccccaagacagacgaagtgtgtggcaacgccttctcgagagcgtgcataggcgccc	448
Db	98	ITTCACACCCACACAGACAGATGTGGACACCGGTTTGTGCGCAGACATGCATCCGTGTC	157

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 Db 572 AACACCTGCTGT 631
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 Db 1522 CATTCTGTTTGAAGATGCAAGAACGCTTACATTAAGATGACACTGTGTTCTTGAA 1581
 QY 1879 gtcatagtagatctcagatcgt 1919
 Db 1582 GTGGCGGTGACTTAACCTGACCTGAGAGATCTTACTACT 1622

RESULT 13
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 ACCESSION AB000509
 VERSION AB000509.1 GI:2982670
 KEYWORDS TRAF5.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 3993)
 AUTHORS Mizushima, S.
 TITLE Direct Submission
 JOURNAL Submitted (16-JAN-1997) to the DBJ/EMBL/GenBank databases. Seichi
 Mizushima, Mochida Pharmaceutical Co., Ltd, Biosciences Research
 Laboratory, 1-1, Kamiya 1-chome, Kita-ku, Tokyo 115, Japan
 (E-mail: smizushim@mochida.co.jp, tel:03-3913-6261)
 2 (sites)
 REFERENCE Mizushima, S., Fujita, M., Ishida, T., Azuma, S., Kato, K., Hirai, M.,
 Otsuka, M., Yamamoto, T. and Inoue, J.
 Cloning and characterization of a cDNA encoding the human homolog
 of tumor necrosis factor receptor-associated factor 5 (TRAF5)
 Gene 207 (2), 135-140 (1998)
 FEATURES
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 JOURNAL
 MEDLINE
 CDS
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 BODCEKHYCAVDKRNIOHHEHSLREHRYLLEKNVLEEDISLHSLSEKES
 KIQCLAEITIKLEKFPKPDLPFGNSFLPRIVQFASHIDSANLEQVHOLLQVY
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BASE COUNT 1198 a 797 c 866 g 1132 t

RESULT 15
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LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AC053507 49960 bp DNA HNG 16-APR-2000
Homo sapiens clone RP11-318L16, LOW-PASS SEQUENCE SAMPLING.
AC053507 GI:7577633
HTG: HTGS_PHASE0.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Waterston, R.H.
1 (bases 1 to 49960)
The sequence of Homo sapiens clone
2 (bases 1 to 49960)
Unpublished
Waterston, R.H.
Direct Submission
Submitted (16-APR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
Center project name: H_NH0318L16.
* NOTE: This record contains 94 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

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347: gap of unknown length
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874: gap of unknown length
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1321: gap of unknown length
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1838: contig of 517 bp in length
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1849
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27380: contig of 504 bp in length
27390: gap of unknown length
27908: contig of 518 bp in length

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 Db 454 GTGATTTAAAAATGATTTGTCATTTTGAAGACTTTCATGTGTGCGCTCGACTGCAA 395
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 QY 670 gaaaggtcttgagaaagacccctgcagacagcttgagaaagcggtgtaataccggg-a 728
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 sequence.
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 VERSION AI344113.1 GI:4081319
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 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: Robert.Strausberg@nih.gov
 Tel: (301) 496-1550
 Tissue Procurement: Ian Kirsch, M.D., Michael R. Emmert-Buck,
 M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
 www.bio.liln.gov/bdrip/image/image.html
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 High quality sequence stop: 448.
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 /clone_id="NCI_CGAP_CO16"
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 /lab_host="DH10B"

FEATURES

SOURCE

1..568
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="2062637"
 /clone_id="NCI_CGAP_CO16"
 /tissue_type="colon tumor, RER+"
 /lab_host="DH10B"

/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
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 Plasmid DNA from the normalized library NCI_CGAP_CO16 was
 prepared, and ss circles were made in vitro. Following HAP
 purification, this DNA was used as tracer in a subtractive
 hybridization reaction. The driver was PCR-amplified cDNAs
 from a pool of 5,000 clones made from the same library
 (cloneids 1057416-106125, and 114584-114531).
 Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 144 a 132 c 111 g 181 t
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 Matches 567; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 Db 28 TAAGTAAAGAGAGATTTATGAATTAAGT 1

RESULT 3
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 VERSION AL135246.1 GI:6603433
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Ansoorge, W., Winkler, U., Mewes, W., Well, B. and Wiemann, S.
 EST (Ansoorge, W., Winkler, U., Mewes, H.W., Well, B. and Wiemann, S.)

JOURNAL
COMMENT On Apr 7, 1998 this sequence version replaced g1:3035257.

Unpublished (1999)
On Apr 7, 1998 this sequence version replaced g1:3035257.
Contact: Ansgore W
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Mleemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ). Email: s.wleemann@dkfz-heidelberg.de;
Sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No si sequence available.
This clone (DKFZ/62M1613) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcentzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

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/db_xref="taxon:9606"
/clone="DKFZ/62M1613"
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BASE COUNT 176 a 129 c 139 g 143 t
ORIGIN

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Matches 585; Conservative 0; Mismatches 2; Indels 3; Gaps 2;

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DB 1 GCTGATGATCAGGGGTCCCTCGCAGCTATTGGAGATGATCAAGCCGACCCCA 60
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QY 1878 agtcatatgtagtactcggatcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1937
DB 181 AGTCATAGTGATGATCTCGATCTGCCGATCCCTGATAGTACGTGGGAGGTGATTT 240
QY 1938 agcagaagcgaactcctcctgggggatttgaaccggtctgtctcactgagtcgcgcgc 1997
DB 241 AGCAGAAGCGAACCTCCTGGGGGATTGACCGGCTCTCTTCACGTAGGTCCTGGC 300
QY 1998 tcagaagaagcacttctgagacgagagcagcgagcagcgagcgagcgagcg 2057
DB 301 TCAGAAAGAGCACTTGTGAGACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
QY 2058 gagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2117
DB 361 GAGCAGCAGCGGTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 420
QY 2118 gaattatattcctcacaagaataatctgctcagaagaagcttcatttcaatt 2177
DB 421 GAATTATTTATCTTCACAAAGATTAATTTGCTGTCAGAGAGGTTTTCATTTTCA 480
QY 2178 ttaagaatcagcttaataagctgagaaacataatgctcctaaacaaagaacatgatt 2237
DB 481 TTAAGATCTTACTTATTAAGGTGAGAAACATATATGCTAAACAAAGAAACATGATTT 540
QY 2238 tcttccttaacttgaacacacacacacacacacacacacacacacacacacac 2287
DB 541 --CTCCTTAACTTGAAACAC--AAAAAACACACACACACACACACACACACG 587

RESULT 4

AI582315/c 661 bp mRNA EST 14-DEC-1999
LOCUS t96606.x1 NCI-CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2213771 3'
DEFINITION similar to TR:Q13947 Q13947 CD40-ASSOCIATED PROTEIN.; mRNA
sequence.
ACCESSION AI582315
VERSION AI582315.1 GI:4568212
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS NCI-CGAP
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Index
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
On Oct 30, 1998 this sequence version replaced g1:3814596.

COMMENT

Contact: Robert Strausberg, Ph.D.
Tel.: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbp/image/image.html
Insert length: 719 Std Error: 0.00
Seq primer: -40UP from Glbco
High quality sequence stop: 426
POLYA-NO.

FEATURES

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2213771"
/clone_id="NCI-CGAP_Lu19"
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differentiated (4 pooled tumors, including primary and
metastatic)"
/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/note="Organ: Lung; Vector: pRT3D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
pooled lung tumor tissue, and was then primed with a Not I
- oligo(dT) primer. Double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pRT73 vector. Library went through one round of
normalization. Library constructed by Bento Soares and M.
Fatima Bonaldo."

BASE COUNT

164 a 147 c 131 g 219 t
ORIGIN

Query Match 22.0%; Score 513.8; DB 41; Length 661;
Best Local Similarity 97.4%; Pred. No. 4.1e-125;
Matches 554; Conservative 0; Mismatches 12; Indels 3; Gaps 3;

QY 1771 aagaagccacacgagagatgatcgcctctgctgcccagctcttggggcccaact 1830
DB 661 AAGAAGCCACACGAGAGATGAT--TCGCTCTGCTGCCAGTCTTGTGGCCCAACT 603
QY 1831 gttcagaagaatgagacataataaagatgatacatttttaagaatcagtgat 1890
DB 602 GTTCAGAAATGGGACATATTTAAAGATGAT--CATTTTATTAAGTCAATATGAT 544
QY 1891 actcgatctgcccagatccctgataagtagctgggaggtgagattagcagaagcaac 1950

Db	543	ACATC-GATCTGCCCCGAGCAGAGACAAAGTACGGGGGAGGTGGATGGATACCAACAAGCAAC	485
Qy	1951	tcctctgaggatttgaaacccggtctgtcttctacttgaagtccttcgcgtctagaagaaagacc	2010
Db	484	TCTCTGGGGGATTTGAAACCGGTCGTCTCACTGAGGTCTTCGGCCTCAGAAAAGAAC	425
Qy	2011	ttgttgagacgggaagacgcggacgaaggcggagacgtgcgcggcgaggagacacgcgagaa	2070
Db	424	TTGTGAGACGGAGGAAACGGGAGAGGCGGAGCGACGTCGGCGGGAGGAGCAACCGCTGA	365
Qy	2071	gcaacactgacacglttctaataatagctagccaaacttaactcttgaagaattattatcc	2130
Db	364	GCACACCTGACACGCTTTTAAATGATAGACTACCACTTCACTCTGAGAAATATTATTAC	305
Qy	2131	ttcaacaagataaattatgtctgtcagaggaagtttcatattcattttaaagaatcgt	2190
Db	304	TTCAACAGATTAATATTGCTGTCAGAGGATTTTCATTTCATTTTAAAGACTCTAGT	245
Qy	2191	taattaaagtgbaaaacatatatgtctaaacaaaagaacatgatlttcttccctaaact	2250
Db	244	TAAATTAAGGTGGAAACAATATATGCTTAACAAAAGAAACATGATTTTCTTCTTAACT	185
Qy	2251	tgaacaccaaataaaacacacacacacacacacacgctggggagtagtgaacatgfcacaatgt	2310
Db	184	TGAACCCCAAAAACACACACACACACACACCTGGGGATAGCTGACATGTCCACCATGT	125
Qy	2311	taagtaaaaggagattcatgaaatagta	2339
Db	124	TAACTAAAGAGAGATTTATGAAATAGTA	96

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RESULT 5
AM081351/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AM081351 563 bp mRNA EST 14-OCT-1999
xc41b10.x1 NCI-CGAP.CO20 Homo sapiens cDNA clone IMAGE:258611 3'
Similar to TR:Q13947 Q13947 CD40-ASSOCIATED PROTEIN. ;contains
Ltr1.t2 LTR1 repetitive element ;, mRNA sequence.
AM081351
AM081351.1 GI:6036503
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 563)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA library preparation: Life
Technologies, Inc. cDNA library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdrrp/image/image.html

Possible reversed clone: polyt not found
Seq primer: -40up from Gtbo
High quality sequence stop: 427.
Location/Qualifiers
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/clone_image="IMAGE:258611"
/clone_id="NCI-CGAP.CO20"
/tissue_type="moderately differentiated adenocarcinoma"
/lab_host="DH10B"
/note="Organ: colon; Vector: pCMV-SPORT6; site_1: SalI;

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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.	
Normalized to Cot 500. Average insert size 1.11kb.	
Normalized version of NCI-CGAP_Col08. Library constructed	
by Life Technologies."	
BASE COUNT	125 a 149 c 132 g 157 t
ORIGIN	

Query Match	Similarity	21.2%	Score 495.8	DB 63	Length 563
Best Local	Similarity	98.3%	Pred. No. 2.2e-120		
Matches	522	Conservative	0	Mismatches	7
				Indels	2
				Gaps	2
QY 1369	catgacacgaatctgagttgtgcacgacatccgcctcagccgacatggacattgagcttgccttcag	1428			
Db 563	CATTGACCAATGCTGTAGTGTGCACGACATCCGGCTTAGCGACATGGACCTGGCCTTCAG	504			
QY 1429	gtccttgagacgcgcgcacgtacaaatggagtgtcaatcttggaagaattcgacataacgcg	1488			
Db 503	GTCTCGAGAACCG-CAGCTACAAATGAGTGCCTCATCTGTGGAAGATTGGCGACTCAAGCGG	445			
QY 1489	cggaagcaggaagggccgtctctggggaagaccttccctttacggcgaagcctttctacat	1548			
Db 444	CGGAAGCAAGAGGCGCTCATGGGGAAGCCCTTCCCTTTACAGCAAGCCTTTCTTACT	385			
QY 1549	ggtaactctgtgcataaagattgtgtgcaggggtctacactgaacggagggagatggggaa	1608			
Db 384	GGTACTTGGGTATATAGATGTGTGCCAGGGTCTACTGTGAACGGGGAAGGGGAG	325			
QY 1609	gggaagcactgtgtcgtgtttttttgtcaatcagtcggtggagaataatgatacctgtcct	1668			
Db 324	GGGAGCCACTGTCTGCTGTGTTTGTTCATCATCTCGTGGAATAATGATGCTGCCCTCC	265			
QY 1669	tggcc-gtttaagcagaagaatgacactctatctgcattgagatcagaagggtcccttcagctca	1727			
Db 264	TGGCCGTTTAAGCAAAAGATGACATCATGCTGATGGATCAAGGGGCTCTGTGACGTCA	205			
QY 1728	tttgaggagatgcatltaagaagccgcaccccaacagcagcagcttcaagaagaccactgaga	1787			
Db 204	TTTGGGAGATGCAATTCGAAGCCGACCCCAACAGCAGAGCTTCAAGAAAGCCCTGAGA	145			
QY 1788	gatgaatctgcctctgtcgtgtccagatcttgtggcccaactgctctagaataatggag	1847			
Db 144	GATGATATCGGCTCTGCGGTGCGCCACTCTTTGGGGCCCAACGTCTTAAGAAATGGGAC	85			
QY 1848	ataataaagatgtatatacaatttttaataatcatagttgatacttcgga	1898			
Db 84	ATATATTAAGATGATACCATTTTATTAAAGTCATGATGATACCTTCGAA	34			
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LOCUS	AA625253	529 bp	mRNA	EST	15-OCT-1997
DEFINITION	a166b04.r1 Soares_Nhmmp2-S1 Homo sapiens CDNA clone IMAGE:1047151				
	5' similar to TR:G695358 G695358 CD40-ASSOCIATED PROTEIN. ; mRNA				
	sequence.				
ACCESSION	AA625253				
VERSION	AA625253.1	GI:2537638			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
REFERENCE	1 (bases 1 to 529)				
AUTHORS	Hillier, L., Allen, M., Bowles, L., Dubuque, T., Gelsel, G., Jost, S.,				
	Kirizman, D., Kucada, T., Lacy, M., Le, N., Lennon, G., Mair, M.,				
	Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,				
	Theising, B., White, Y., Wyllie, T., Waterston, R., and Wilson, R.				
TITLE	WashU-NCI human EST Project				
JOURNAL	Unpublished (1997)				
COMMENT	On Jan 17, 1998 this sequence version replaced gi:1900639.				
	Contact: Wilson RK				
	Washington University School of Medicine				
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108				

QY 475 acagcgtgtcaagagagcgtcttaagataaggtgtttaaggaataattgtctgcagaga 534
 DB 312 ACAGGCTGTCAAGAGAGCATGCTTAAGATAGGTTTAAGGATATGCTGCAGAGA 253
 QY 535 gaattctgtctcttcacatctatctgtcggaatgaagcagaggttgcagagcagta 594
 DB 252 GAAATTCGGCTCTTCAGATCTATTTGTGGAAAGAGAGGTTTGCAGACAGCTTA 193
 QY 595 atgcctggagacat---ctgtgcatcttaaaatgaattgccatttgaagaattccatgt 651
 DB 192 ACCTGGGACATCTCTGCTGATTTAAATAATGATGCTTGAAGAACTTCATGT 133
 QY 652 gtgcgtctgtcgtcgaagaaaggctcttgagaaagacctgcagagcagctggagaag 711
 DB 132 GTGCTCTGTGATGCAAGAAAGAGCTTGAAGAAAGCTGCAGACACTGGAGAG 73
 QY 712 gctgttaataacccgggaagccacatgcagccactgcagagagtcaggttcgatgcgcg 771
 DB 72 GCGTGAATATCCGGGAAGCCACATGCAGCCACTGCAAGAGTCCAGTTCGATCG-G 14
 QY 772 ctgcgaaacacg 784
 DB 13 CTACAGAAACAG 1
 RESULT 8
 AA194061/c 658 bp mRNA EST 14-FEB-1997
 LOCUS z137d03.r1 Soares_NHMPU.S1 Homo sapiens cDNA clone IMAGE:65573 5'
 DEFINITION similar to TR:G695358 G695358 CD40-ASSOCIATED PROTEIN. ;, mRNA
 sequence.
 AA194061
 AA194061.1 GI:1783807
 EST.
 human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 658)
 HALLIER, L., CLARK, N., DUBUQUE, T., ELLISTON, K., HAWKINS, M.,
 HOLMAN, M., HULTMAN, M., KUCABA, T., LE, M., LENNON, G., MARTA, M.,
 PARSONS, J., RIFKIN, L., ROHLFING, T., SOARES, M., TAN, F.,
 TREVAKKIS, E., WATERSTON, R., WILLIAMSON, A., WOLDMANN, P. and
 WILSON, R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 CONTACT: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LML; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Possible reversed clone: similarity on wrong strand
 High quality sequence stop: 327.
 FEATURES
 Source
 Location/Qualifiers
 1..658
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 /db_xref="GDB:5427605"
 /db_xref="taxon:9606"
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 /clone_lib="Soares_NHMPU.S1"
 /tissue_type="Pooled human melanocyte, fetal heart, and
 pregnant uterus"
 /lab_host="DH10B"
 /note="Organ: mixed (see below); Vector: p7T73D-Pac
 (Pharmacia) with a modified polylinker; Site: 1: Not 1;
 Site 2: Eco RI; Equal amounts of plasmid DNA from three
 normalized libraries (melanocyte 2NBH19, pregnant uterus
 NBHPU, and fetal heart NBH19W) were mixed, and ss circles
 were made in vitro. Following HAP purification, this DNA

was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from pools of
 5,000 clones made from the same 3 libraries. The pools
 consisted of I.M.A.G.E. clones 260232-265223,
 340488-345479, and 484488-489479.
 BASE COUNT 143 a 173 c 155 g 176 t 11 others
 ORIGIN
 Query Match 19.1% Score 446; DB 22; Length 658;
 Best Local Similarity 91.6%; Pred. No. 3.5e-107;
 Matches 589; Conservative 0; Mismatches 39; Indels 15; Gaps 11.
 QY 154 gtccctactctcttcaagatgcgtctctgacaaagaagacatcccttccataaag 213
 DB 647 GCTCCCTACTCTCTTAAGA-NGCTTTNTGACAAAGGAACCTTTCTTCNTAATG 589
 QY 214 gattcgagtaaaagatgacac-tcctggcgcgctgcagactaa-ccgcgcgtaaagc 271
 DB 588 GAGTCGAGTAAAGATGAGACTTCTTCTGCGCNGCTTCAGACTAACCCGCCCTAAAGC 529
 QY 272 tgcacactgaccg-caatgctcggagcgccagtttttgccttgacaaagaggttaacag 330
 DB 528 TNCACACTGACCCNCCAGTGTGAGACCCCAAGTNTTGTCCCTGAACAAGAGGTACAG 469
 QY 331 gaaagtttgtg-aagaccgtggaagac--aagtaaaagtgtgaagttgac--accctg 385
 DB 468 GAAAGTTTGTGAAGAACCGCTGAGAGACCAAGTACCAAGTGTGAGAAATGCCCACTTGG 409
 QY 386 tgcgttg-caagcccgacagacagcagatgtggc-accgctctgc-gagagctcatgg 442
 DB 408 TGCTGTGCCAGCCGGAACAGACAGCGAGTGGGCAACCGCTTCTCGGAGAGCTCATAGG 349
 QY 443 cggccctgtgagctcttcaagtcacaaatgtaacgctgtcagaagagcagtcgttaag 502
 DB 348 CGGCCCTGCTGAGCTCTTCAAGTCCAAATGTACAGCTGTCAAGAGAGCATCGTTAAG 289
 QY 503 ataaagtgttaagatattgtctgcagagagaagaattcgtcttcaagatattgtc 562
 DB 288 ATAAAGTTTAAAGATATGCTGCAAGAGAAATTTGCTCTTCAAGATATTTGTC 229
 QY 533 ggaatgaagaagaaggtgtgtcagagcagtaattgtgtgaac--ctgtgtcatlaa 619
 DB 228 GGAATGAAGAAGAGGTGTGTGCAAGAGATTAAAGCTTGACATGTGCTGTGCAATTAA 169
 QY 620 aaaaatgtccatttgaagaacttccatgtgtgtcgtcgtcgtcgtcgtcgtcgtcgtc 679
 DB 168 AAAATGATTCATTTTGAAGAACTTCATGTGTGCTGTGCTGCAAGAAAGTCT 109
 QY 680 tgaagaagaactcgtgcagacacagctgtggaagagcgctgtaataaccgggaagccaatca 739
 DB 108 TGAGGAAAGACCTCGGAGACCACTGGAAGGCGCTGAATACCGGGAAGCCACATGCA 49
 QY 740 gccactgaagatcaggttcgcgatgcgcgcgtcagaaca 782
 DB 48 GCCACTGCAAGAGTCAAGTTCGATGANTCCGCTGCAGAAACA 6
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 DEFINITION similar to TR:Q13947 Q13947 CD40-ASSOCIATED PROTEIN. ;, mRNA
 sequence.
 AW589978
 AW589978.1 GI:7277103
 EST.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 404)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution Information can be
found through the I.M.A.G.E. Consortium/LINL at:
Image.lnl.gov/Image/html/lresources.shtml
Seq primer: -40UP from Gibco.

FEATURES
SOURCE
Location/Qualifiers

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/clone="IMAGE:2946911"
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/tissue_type="Pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: pUT73D-Pac (Pharmacia) with a modified
polylinker; plasmid DNA from the normalized library
polylinker; plasmid DNA was prepared, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from a pool of 5,000 clones made
from the same library (clonoids 1257096-1258631,
1469064-1470983, and 1475592-1476743). Subtraction by
Bento Soares and M. Fatima Bonaldo."

BASE COUNT 101 a 109 c 93 g 101 t
ORIGIN

Query Match 17.3%; Score 404; DB 74; Length 404;
Best Local Similarity 100.0%; Pred. No. 3.8e-96;
Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1481 aaaaacggggaagcagcagcgcgttcatacgtggaagaccccttccttcacagccagccct 1540
DB 404 ACAAAGCGGCGAAGCGAGGCGCGTATGGGAAGACCTGTCCTTTCACAGCCAGCCTT 345
QY 1541 tctaaccttgcttacttgctgctataagatgtgtccagggcttactcctgaacggggaagc 1600
DB 344 TCTACACTGCTTACTTGTGCTATAGATGTGCGGCGTCTACCTGGAAGGCGGAGCGGA 285
QY 1601 tggggaagggagcagcagcctgtcgctgtttttgtcatcatgctgtgagaataatgagccc 1660
DB 284 TGGGGGAAGGGAAGCGCACTTGTGCTGCTTTTGTTCATCATGCTGGAGAATATGATGCC 225
QY 1661 tcttccttgccgctttaagcagaagtgacactcatgctatgatagtcaggggtctcttc 1720
DB 224 TGTCTTCTTGCGCGTTTAAGCAGAAAGTGAACACTCATGCTGATGATGATCAGGGGTCTCTC 165
QY 1721 gacgtcatttgggagatgcatcattcaagccgcaaccccaacagcagcagcttcaagaagccca 1780
DB 164 GACGTCATTGGGAGATGATCAAGCCGAGCCCAACAGCAGCAGCACTTCAAGAAACCCA 105
QY 1781 ctggagagatgataatcgcctcgtgctgcccagcttttggcccaactgtttctagaaa 1840
DB 104 CTGGAGAGATGATATCGCTCTGCTGCCACTTCTTTGTGGCCCAAACTGTTCTAGAAA 45
QY 1841 atgggacataataaagatgatacaatttttaaaagcata 1884
DB 44 ATGGGACATATATTAAGAATGATACATTTTATTAAGTCATA 1

RESULT 10
AM104914
LOCUS " AM104914 510 bp mRNA EST 20-OCT-1999

DEFINITION xdt2e06.x1 Soares, NFI, T.GBC, SI Homo sapiens cDNA clone
IMAGE:2603170 3' similar to TR:Q13947 Q13947 CD40-ASSOCIATED
PROTEIN. ; mRNA sequence.
ACCESSION AM104914
VERSION AM104914.1 GI:6075649
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 510)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -40UP from Gibco
High quality sequence stop: 407.

FEATURES
SOURCE
Location/Qualifiers

1. 510
/organism="Homo sapiens"
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/lab_host="DH10B"
/note="Organ: pooled; Vector: pUT73D-Pac (Pharmacia) with
a modified polylinker; Site:1: Not I; Site:2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NDHL19W, testis NHT, and B-cell
NCI-CGAP GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT 116 a 149 c 159 g 85 t 1 others
ORIGIN

Query Match 16.1%; Score 377.4; DB 63; Length 510;
Best Local Similarity 97.5%; Pred. No. 4.5e-89;
Matches 425; Conservative 0; Mismatches 7; Indels 4; Gaps 4;
QY 10 acggcccgaggcccttgagcccgccgagcggagcggagcggagatgaggaataatgag 69
DB 75 ACGCCCGCGCGCCCTCGTGGCGCGCGAGCGCGAGCGCGCGAGATGAGAAATGAG 134
QY 70 gcccaagaagtgatgaccccttggttaaggtgtccagagaaggttcagaatcagacctaga 129
DB 135 GCCCAAGAAGTGAATGCCCTTGTTAAGGTCCAGAGAGAGTCAGAATCAACACTAGGA 194
QY 130 tgaagaacctgctcctgctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 188
DB 195 TCAGAAACTGGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 254
QY 189 aagagaacctcctccttctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 248
DB 255 AAGAGAACTCCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 314
QY 249 ggaagtaacccgagcggcgaagcgtcacaactgacccgagcgtgagagccaggttttct 308
DB 315 GCAAGCTTAACCGCGCGCTTAAGCTGACACTGACCGAGTGTCTGGAGCCAGTTTCT 374
QY 309 ccttgacagaagggttacaagaagaagtttgtgaagaccgtggaagcaatgacaagt 368

```

Db 375 CCCTCAACAGAGAGGTTCACAGAAAGTGTGTGAAGACCGTGGAGGACCAAGTACAAAGG 434
Oy 369 tgaagaatgtccacc-tgtgtctgtctgcacgccgaagcaga-ccgaattgtggcga-ccgctt 425
Db 435 TNGAAGATGCCACCTGTGGTGTCTGTCTGACACCCGACAGACAGACCCGAGTGTGGGACCCGCTT 494
Oy 426 ctgcgaagagctgcctcatg 441
Db 495 CTGCAGAGAGCTGATG 510

RESULT 11
LOCUS AI393367
DEFINITION t94e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2111650 3' similar to TR:Q13947 Q13947 CD40-ASSOCIATED
PROTEIN: ;, mRNA sequence.
ACCESSION AI393367
VERSION AI393367.1 GI:4222914
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.
REFERENCE 1 (bases 1 to 477)
AUTHORS MCI-CGAP http://www.ncbi.nlm.nih.gov/mcicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel.: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LINT; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1222 Std Error: 0.00
Seq primer: -40up from Gbco
High quality sequence stop: 322.
FEATURES
Source Location/Qualifiers
1..477
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2111650"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site.1: Not I; Site.2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBH139W, testis NHT, and B-cell
MCI-CGAP-GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687339,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT 113 a 143 c 143 g 78 t
ORIGIN
Query Match 15.4%; Score 359.6; DB 39; Length 477;
Best Local Similarity 95.0%; Pred. No. 2.2e-84;
Matches 382; Conservative 0; Mismatches 19; Indels 1; Gaps 1;
Oy 10 agcggccggcgccccctgagccggcgagcgagcgagcgagcgagatgagaaatgag 69
Db 75 ACGCCCGCGCCGCCCTGTGAGCCGGCGACGGCGACGGACGCCCGAGTAGGAAAAATGAG 134
Oy 70 gcccaagaagatgatcccttggttaagatgccagaagatgcagaatcacagacttga 129
Db 135 GCCCAAGAAGATGATCCCTGTGTTAAGTCCGACAGAGAGTTCAGAAACAACCTTAGA 194
Oy 130 tcagaacctgtctcctgtcctc-gtccctactcttctaagatcgctgtctctagag 188

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Db	195	TCAGAAACCTGGCTCCTGGCTCCTGGCTCCTGACCTTTTAAGATCGCTGCTCAG	254
OY	189	aagagaactcctcttctcctaataatgagtcgagtaaaagatggaactctctgacgct	248
Db	255	AAGAGAACTCCTCTTCTCTTAATGAGTGCAGTAAAGANGAGCACTCCTCGCGGCT	314
OY	249	gcagactaacccgcgcgctaagctcgcacactgacgcgcaatgctggaagccagtttct	308
Db	315	GCAGACTAACCCGCGCTAAAGCTGCACACTACCCCACTGCTGGGACCCCACTTTTGT	374
OY	309	cccttaacaagaaggttacaagaagaagtgttgaaagccgctggaagacaagaatg	368
Db	375	CCCTTAACAAGAGAGGTTCACAGAGAAAGTTTGTGAAGACCCGTCGAGGACAGTACCA	434
OY	369	tgaagaatgcacactgctgtctgtgcagcccggaagcagacga 410	
Db	435	TGAGAAAGTGACACTGGTGTGTGCAACCCCGAAGACAGACGGA 476	
RESULT 12			
LOCUS	N76469/c		
DEFINITION	Y767d10 r1 Soares multiple_sclerosis_2NBHMSp Homo sapiens cDNA	EST	02-APR-1996
ACCESSION	N76469		
VERSION	N76469.1	GI:1239047	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 475) Hallier,L., Clark,N., Dubuque,T., Elliston,R., Hawkins,M., Holman,M., Holtman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trivaslis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.		
TITLE	The WashU-Merck EST Project		
JOURNAL	Unpublished (1995)		
COMMENT	On Jan 6, 2000 this sequence version replaced gi:6676353. Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.wustl.edu This clone is available royalty-free through LNL; contact the IMG Consortium (Info@image.llnl.gov) for further information. Seq primer: reverse ET High quality sequence stop: 291. Location/Qualifiers 1..475 /organism="Homo sapiens" /db_xref="GDB:3905875" /db_xref="taxon:9606" /clone="IMAGE:290035" /clone_lib="Soares_multiple_sclerosis_2NBHMSp" /sex="male" /tissue_type="multiple sclerosis lesions" /dev_stage="Age 46" /lab_host="DH10B (ampicillin resistant)" /note="Vector: pT73D (pharmacia) with a modified polylinker V.type: phagemid; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5]. TGTTACCAATCTGAGTGGAGCGCGCATTTTTTTTTTTTTTTT 3'), double-stranded cDNA was size selected, ligated to Eco RI adapters (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento		

Soares and M. Fatima Bonaldo. RNA from 4 multiple sclerosis lesions from one patient was kindly provided by Dr. Kevin G. Becker (NINDS/NIH).
 BASE COUNT 117 a 121 c 117 g 114 t 6 others
 ORIGIN

Query Match 14.7%; Score 344.8; DB 87; Length 475;
 Best Local Similarity 92.2%; Pred. No. 1.8e-80;
 Matches 427; Conservative 0; Mismatches 27; Indels 9; Gaps 6;

QY 1423 tccacagctctctgaga-cgcacagctacacagctgctcattctggaattcgcgac-t 1480
 DB 464 TTCACAGCTCTCTGAGACCCGCCAGCTACATGNGTCTCATCTCAAGATTCGCCACTT 405
 QY 1481 acaagcgcgcg-aagcagagagcgcgc--atgggagaagccctgctcccttaacagcagc 1537
 DB 404 ACAAGCGGNGAAGACAGAGGCGCCCGCATGGGAAGACCTGTCCCTTACAGCCAG 345
 QY 1538 cttctc---acactgttctctgctataagatgtgtgcagaggtctcctcgaagggg 1594
 DB 344 CTTTCTCAACTGCTTCTTCTTGTGCTATAGATGTGTGCGAGGCTTACCTGAACGGGG 285
 QY 1595 acgagctgggaaagggagcagctgtgcgtgttttgcacatcagctgaggaatg 1654
 DB 284 ACGGAGTGGGGAAGGGAGCGACTTTCGCTGTTTTCATCATCGCGGAGATATG 225
 QY 1655 atgcctgtctccttgcgcgttaagcagaagtgacactcatgctg-atggaacagggg 1713
 DB 224 ATGCCGTGCTCCTTGGCGGTTTAAAGCAGAACTGACACTCMTNCTGAATGATCAGGCT 165
 QY 1714 tctctcgcagctcatttggagagatgattcaagcccgaccccaagcagcagcttcaag 1773
 DB 164 TCCCTCGACGTCATTGTGGAGATGCAATCAACCCGACCAACAGCAGCACTTCAG 105
 QY 1774 aagccacatggagagatgaatcgcctcgtgctgcccagctcttggcccaactgtt 1833
 DB 104 AAGCCACATGAGAGATGATGANTCTCCTGCTGCGCAGCTTTTGGGCCAAGCTGT 45
 QY 1834 ctgaaaatggagacatatattaagaatgatacaattttatta 1876
 DB 44 CTGAAATGGGACATATATTAAGATGATACAAATTTTATTA 2

RESULT 13
 W40768/c 535 bp mRNA EST 11-SEP-1996
 LOCUS mc38d11.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone
 DEFINITION IMAGE:350805.5, similar to gb:U21050 Mus musculus CD40 receptor
 associated factor 1 (MOUSE);, mRNA sequence.
 ACCESSION W40768
 VERSION W40768.1 GI:1325087
 KEYWORDS house mouse.
 SOURCE EST.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 535)
 REFERENCE Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubugue, T.,
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, R., Steptoe, M., Tan, F., Underwood, R., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.
 TITLE The WashU-HMT Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT On Jan 7, 1998 this sequence version replaced gi:933067.
 Contact: Marra M/Mouse EST Project
 WashU-HMT Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LIND; contact the
 IMAGE Consortium (info@image.lind.gov) for further information.
 MG1:222605
 Seq primer: ETPRimer
 High quality sequence stop: 135.
 Location/Qualifiers
 1..535
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:350805"
 /clone_11b="Soares mouse p3NMF19.5"
 /dev_stage="19.5 dpc total fetus"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Vector: pRT3D (Pharmacia) with a modified
 polylinker site. 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5',
 TGTATCCATCTGTAAGTGGAGCGGCGGCGCATTTTCTTTTCTTTT 3'],
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pRT3 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M. Fatima Bonaldo. RNA was kindly provided by
 Dr. Minoru Ko (Wayne State University)."

BASE COUNT 113 a 150 c 132 g 140 t
 ORIGIN
 Query Match 14.2%; Score 332.8; DB 91; Length 535;
 Best Local Similarity 84.5%; Pred. No. 2.9e-77;
 Matches 399; Conservative 0; Mismatches 67; Indels 6; Gaps 2;

QY 202 ttctctaaatgagctgagtaaaagtgtgactctcgtgagcgtgagactaacccg 261
 DB 469 TTTCTTAAGATGAATCAAGCAAAAAGATGATTTGCTCGACACTGACCTTAACCA 410
 QY 262 ccgctaaagctcacactgaccgagctcgtgagagccagcttctgctccctgaacagga 321
 DB 409 CCCCTTAAGCTCAGCGCTATATGCGGCGCAGG---GTGCGTCTGCTGCGGAGCAAGA 353
 QY 322 gtttacaagaaagtgtgtgaagacgtgtgagagcaagtgtgtgaagatgtgccac 381
 DB 352 GGTACAAAGCAAGATTGTGTAAGACCGGTGAAGCAACTACAAATGTCAGAGGCCCC 293
 QY 382 ctggtgtgtgtgagcccgagagacagagtggtggacacgcttctgagagctgcatg 441
 DB 292 CTGGTCTGTTTAACCCGGAAGCAGAGGATGTGGCCACCGGTTTCTGCGAGCTGCA 233
 QY 442 gcgacctgtgagctctcctcaagtcocaaatgtacagcgtgtcagaagagacatgttaa 501
 DB 232 GACGCCCTCTGAGCTCCCTCCAGTCCAAATGAGCAGCGTGCAGAAATCATCATCA 173
 QY 502 gataaggtgtttaaagataattgtgtcagaagagaaattctgtctcttaagatcatgt 561
 DB 172 GACAAGGTGTTTAAGGATTAATGCTGCAAGAGAGATTCGCTTCAGCTCACTGT 113
 QY 562 cggatgaagagagaggtgtgtcagagcaggttaagctgtgagacat---ctgtgtcatta 618
 DB 112 CGGAATGAAGGAGAGGTTGTGCGAGCAGCTGACTCTGGACATCTGCTGTGACCTA 53
 QY 619 aaaaatgattgcatattttaaagaacttcatgtgtgtcgtcactgtacaaag 670
 DB 52 AAAAAATGATGTCAGTTTGAAGAACTTCCCTGTCTGCGTCCGAGCTGCAAG 1

RESULT 14
 AA504259 404 bp mRNA EST 18-AUG-1997
 LOCUS aa61b08.s1 NCI-CCAP GCB1 Homo sapiens cDNA clone IMAGE:825399.3
 DEFINITION similar to TR:665358 G695358 CD40-ASSOCIATED PROTEIN.;, mRNA
 sequence.
 ACCESSION AA504259
 VERSION AA504259.1 GI:2240419

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 404)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Oct 31, 1997 this sequence version replaced gi:1520960.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.linnl.gov/dbp/image/image.html

FEATURES
source
Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
1..404
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:825399"
/clone_id="NCI_CGAP_GCB1"
/issue_type="germinal center B cell"
/lab_host="DH10B"
/note="Vector: pRT3D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, 19D-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). CDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAGGAGGCGGCGCTCATTTTTTTTTTTT-3'
]. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pRT3D vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 104 a 109 c 121 g 70 t
ORIGIN

Query Match 13.1%; Score 305.8; DB 27; Length 404;
Best Local Similarity 98.8%; Pred. No. 3.6e-70;
Matches 329; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 41 ggcagcgacgcgagatgaggaatgagcccaagaagtgtaccctgttaagt 100
DB 73 GCATCGGACCCCGAGATGAGGAATGAGGCCCAAGAAGTATGCTTAAAGT 132
QY 101 cccgagaaggtcagaatcagaccctagatcagaactgtgtcgtcct-gtccc 159
DB 133 CCCAGAGCAGGTCAGAAATCAGACTGAGTCAAACTGCTGCTGCTGCC 192
QY 160 tactcttaagatcgtctgtctacagaaagaaactctcttccttaaatgagtc 219
DB 193 TACTCTTTAAGGATCGCTCTCAGAGAAAGAACTCTTCTTAATAATGAGTGC 252
QY 220 agtaaaagaatgagctctcgtcgagctgcagactaacgcgcgttaagtcacact 279
DB 253 AGTAAAGAGATGAGACTCTCTGCGCGCTGACAGTAACTCCCGCTAAAGCTGCACACT 312
QY 280 gaccgagtgctgggagccagttttgtccctgaaagaagaggttaagaagaagttt 339

DB 313 GACCGACTGCTGGGACGCCA-TTTTCTCCCTAACAAGAGGTACAGAAAAAGTTT 371
QY 340 gtaagacccgtgagagacagataagtgtag 372
DB 372 GTGAAGACCGTGGAGGAGCAAGTACAGAGTGTAG 404

RESULT 15
A1549245
LOCUS
DEFINITION UT-R-C3-1x-d-02-0-UI-s1 UT-R-C3 Rattus norvegicus cDNA clone
UT-R-C3-1x-d-02-0-UI-3', mRNA sequence.
ACCESSION A1549245
VERSION A1549245.1 GI:4466733
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 407)
AUTHORS Bonaldo, M.F., Lennon, G., and Soares, M.B.
TITLES Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT On Jul 19, 1995 this sequence version replaced gi:2939456.
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA library preparation: M.B.
Soares lab clone distribution: clones will be available through
Research Genetics (www.resgen.com) This clone is also available
through the I.M.A.G.E. Consortium at LINL (infoimage.linnl.gov).
IMAGE ID=1755915 The following repetitive elements were found in
this cDNA sequence: 164-216, >(GGA)n#Simple_repeat
Seq primer: M13 Forward
POLYA-No.

FEATURES
source
Location/Qualifiers
1..407
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-C3-1x-d-02-0-UI"
/clone_id="UI-R-C3"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pRT3D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; The UI-R-C3
library is a subtracted library of a series, ultimately
derived from a mixture of individually subtracted normalized
libraries from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, and 8, 12 and 18-day
embryos, after a series of subtractions to reduce the
representation of cDNAs from which ESTs had already been
generated. The following serially subtracted libraries
were generated in this process: UI-R-C3, UI-R-C2P,
UI-R-C1, UI-R-C0, UI-R-A1, UI-R-E1. The tag is a string of
3-5 nucleotides present between the Not I site and the
oligo-dT track which allows identification of the library
of origin of a clone within the mixture. The subtracted
library (UI-R-C3) was constructed as follows: PCR amplified
cDNA inserts from UI-R-C2P clones from which 3' ESTs had
been derived was used as a driver in a hybridization with
the UI-R-C2P library in the form of single-stranded
circles. The remaining single-stranded circles (subtracted
library) was purified by hydroxyapatite column

1	2337.4	99.9	2339	1	T35251	Full-length CD40 b
2	2282.2	97.6	2918	1	T90123	Human CRAP1 (TRAF-
3	2238.8	95.7	2359	1	T31273	LMPI associated pr
4	2038	87.1	2240	1	T30773	CD40 associated pr
5	358	15.3	2105	1	T88022	Murine TRAF5 CDNA..
6	358	15.3	2254	1	T87039	DNA encoding murin
7	314.2	13.4	2846	1	T87040	DNA encoding human
8	313.8	13.4	3993	1	T88023	Human TRAF5 CDNA..
9	155.2	6.6	2380	1	T313273	Epstein-Barr induc
10	153	6.5	2121	1	T12262	Mouse TRAF2 CDNA.
11	140.2	6.0	2088	1	T11261	Mouse TRAF1 CDNA.
12	90	3.8	2004	1	T86169	Human CAR1 nucleo
13	60.4	2.6	2248	1	T88390	Tumour necrosis fa
14	42.4	1.8	17425	1	X28366	Human Stat6 gene..
15	41.4	1.8	1893	1	V13119	Synthetic B. thuri-
16	41.4	1.8	666	1	T36496	Maize glutathione-
17	40.8	1.7	8905	1	X20263	Borrelia burgdorfe
18	40	1.7	1151	1	X21216	Human secreted pro
19	39.8	1.7	2107	1	O46124	Human receptor (EP3
20	39.8	1.7	110000	1	X20248_03	Continuation (4 O5
21	39.4	1.7	44453	1	X23519	Human kidney amino
22	39	1.7	340	1	O37286	DNA encoding SSP-5-
23	39	1.7	7063	1	X24751	Human interleukin-
24	39	1.7	7812	1	X24753	Human interleukin-
25	38.2	1.6	1405	1	O46153	FE2 receptor (EP3)
26	37.6	1.6	44377	1	T78508	Platanolide synthn
27	37.6	1.6	44377	1	T80414	Platanolide synthn
28	37.6	1.6	110000	1	X20248_04	Continuation (5 O5
29	37.6	1.6	116277	1	X20249	Borrelia burgdorfe
30	37.4	1.6	2058	1	V07560	Noccellimastix pat
31	37.2	1.6	1456	1	V43022	Streptococcus pneu
32	37.2	1.6	2356	1	V52355	Streptococcus pneu
33	37	1.6	6175	1	T34291	Coding sequence id

C:\Program Files\Internet Explorer\IEXPLORE.EXE

[illegible]

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|||||
Db 241 GCGGCGCTGCAACTAACCCGCGCTAAAGCTGACACTGACCGGAGTCTGCGAGCCCA 300
Oy 301 gtttttgcctcgaagaagaagttacaagaagaattgtgaagaacgttgagaacaag 360
Db 301 gtttttgcctcgaagaagaagttacaagaagaattgtgaagaacgttgagaacaag 360
Oy 361 tacaagtgtgaagtgtccactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 420
Db 361 tTCAAGTGTGAAGAGTGCACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
Oy 421 cgtcttcgagagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 480
Db 421 CCTCTGTGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
Oy 481 tgtcaagaagagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 540
Db 481 tGTCAAGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
Oy 541 ctgtcttcagatctattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 600
Db 541 CTGCTCTTCAATCTATTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
Oy 601 ggaacatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 660
Db 601 GGACATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
Oy 661 gactcgaagaagaagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 720
Db 661 GACTCTCAAGAAAGAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Oy 721 taacgggaagccacatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 780
Db 721 TACCGGGAAGCCACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
Oy 781 caagaagaacacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 840
Db 781 CACGAAGACACCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
Oy 841 actcctcggagagagagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 900
Db 841 ACTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
Oy 901 tgaatttaagcgtatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 960
Db 901 TGTATTTTAAGCGGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
Oy 961 gaagccagctccgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1020
Db 961 GAGGCCAGCTCCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
Oy 1021 aagaaggttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1080
Db 1021 AAGAAGGTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1080
Oy 1081 cacaatcagatagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1140
Db 1081 CACATTCAGATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1140
Oy 1141 aatgaatcaaaatccctcaatcctacagcagtgatagacagcagaagcagaactgaag 1200
Db 1141 AATGATCCAAATCTTCAATTCATACAGCAGATGACAGCAGCAGAGAAATGTGAAG 1200
Oy 1201 gagcttgaagaagatcgcgcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1260
Db 1201 GAGCTTGAAGAAGATCGGCCCTTCCGGCAGAACTGGGAGAGAGACAGCTGAAG 1260
Oy 1261 agcagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1320
Db 1261 AGCAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1320
Oy 1321 gggcgaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1380
Db 1321 gggcgaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1380

|||||
Db 1321 GGGCAAGTGGCTCGGACACAGGCGCTGTGGAGTCCAGCTGAGCGCGCATGACAGATG 1380
Oy 1381 ctgagtgtgaacagatccgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1440
Db 1381 CTGAGTGTGACAGCATCCGCTTACCGACATGTGACCTCGGCTTCCAGGTCTGTGAGACC 1440
Oy 1441 gccactacaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1500
Db 1441 GCGACTCAATGTGAGTCTCTATCTGTGAAGATTGCGGACTACAGCGCGGAGAGAGAG 1500
Oy 1501 gccgtcatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1560
Db 1501 GCCGTATGGGAGAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1560
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Oy 1621 tgcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1680
Db 1621 TCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680
Oy 1681 cagaagtgacactcatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1740
Db 1681 CAGAAAGTGAACATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1740
Oy 1741 ttcaagccccgagccccagaagcagcttcaagaagaagccccatgtgtgtgtgtgtgt 1800
Db 1741 TTCAAGCCCCGAGCCCCAAGAGAGAGCTTCAAGAGCCCACTGTGAGATGAATATCC 1800
Oy 1801 tctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1860
Db 1801 TCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1860
Oy 1861 gatacaatttataaagtcatagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1920
Db 1861 GATACAATTTTATTAAGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1920
Oy 1921 gctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1980
Db 1921 GCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1980
Oy 1981 cactgaagtcctcgcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2040
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Oy 2041 acggtgtcggcgggagagagccacgcgagagacacacgtgtgtgtgtgtgtgt 2100
Db 2041 ACGGTCGCGCGGGAGAGCGCACGCGAGACACACCTGACACGTTTATATAGACTAG 2100
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Db 2101 CCACCTTCACTCTGMAAATTTATTTATCTTCAACAGATGAATATATGTGTGTGTGT 2160
Oy 2161 gtttcaatttcaattttaaagatctagtttaataagtgtaaaacatatatgtctaac 2220
Db 2161 GTTTCAATTTTCAATTTTAAAGATCTAGTAAATTAAGTGTGAAGAACTATATGTCTAAC 2220
Oy 2221 aaagaanaacatgatlttctcctttaaacttgaacacccaataaacacacacacac 2280
Db 2221 AAAAGAAACATGATTTTCTTCTTAACTTGAACACCCAAAACACACACACACAC 2280
Oy 2281 acgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2339
Db 2281 ACGTGGGATAGCTGTGACATGTCTAGCATGTTAAGTAAAGAGATTTATTAATATGTA 2339

```

RESULT 2

T90123

ID T90123 standard; cDNA; 2918 BP.

AC T90123;

DT 27-MAR-1998 (first entry).

DE Human CRAF1 (TRAF-3) cDNA.

KW	CD40 receptor associated factor 1; CRAFI; TRAF-3; p70; p5; p15;
KW	p55; p55delta9; p70delta9; p55delta9_10; p70delta9_10; p55delta8_9;
KM	p80delta8_9; human; CD40 mediated intracellular signaling;
KM	organ rejection; allergy; hay fever; autoimmune disease;
KM	rheumatoid arthritis; systemic lupus erythematosus;
KM	myasthenia gravis; idiopathic thrombocytopenia purpura;
KM	Graves' disease; haemolytic anaemia; diabetes mellitus; psoriasis;
KM	hyper immunoglobulin E syndrome; apoptosis; infectious disease;
KM	Richter's syndrome; spondyloarthritis; Lyme disease; HIV; syphilis;
KM	tuberculosis; arthritis; scleroderma; fibrosis; pulmonary fibrosis;
KM	pneumococcosis; adult respiratory distress syndrome; pneumonitis;
KM	asbestosis; silicosis; Farmer's lung; hepatitis; cirrhosis;
KM	atherosclerosis; multiple sclerosis; glomerulonephritis;
KM	glomerulosclerosis; glomerulopathy; kidney disease; nephropathy;
KM	endocarditis; leprosy; malaria; Goodpasture's disease;
KM	Henoch-Schoenlein purpura; polyarteritis; multiple myeloma;
KM	Wegener's granulomatosis; cryoglobulinemia; myeloma;
KM	Waldenstrom's macroglobulinemia; amyloidosis; Sjogren's syndrome;
KM	AIDS; oesophageal dysmotility; inflammatory bowel disease;
KM	bladder disease; Epstein-Barr virus; mononucleosis; B cell tumour;
KM	Burkitt's lymphoma; nasopharyngeal carcinoma; pneumonia;
KM	gene therapy; diagnosis; ds.
OS	Homo sapiens.
FH	Key
FT	Location/Qualifiers
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FT	/note= "no exon 2 in p5 coding sequence"
FT	169..545
FT	/tag= p
FT	CDS

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FT CDS 169..2384
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FT sequence"
FT CDS 169..2384
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FT /product= p70del8_9
FT /note= "no exons 8 or 9 in p70del8_9 coding
FT sequence"
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FT /tag= t
FT /product= p55 (CRAF1-a, p60 isoform)
FT 675..2384
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FT /product= p55del9
FT /note= "no exon 9 in p55del9 coding sequence"
FT CDS 675..2384
FT /tag= v
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FT CDS 675..2384
FT /tag= w
FT /product= p55del8_9
FT /note= "no exons 8 or 9 in p55del8_9 coding
FT sequence"
FT W09734473-A1.
PN 25-SEP-1997.
PE U05076.
PR 18-SEP-1996; US-026584.
PR 21-MAR-1996; US-013820.
PR 01-MAY-1996; US-016626.
PR 01-MAY-1996; US-016659.
PA (UYCO ) UNIV COLOMBIA NEW YORK.
PI Cleary AM, Frank DM, Lederman S;
P1 MPI: 97-479907/44.
DR P-PSDB; W27428-37.
PT Protein comprising CRAF1-b domain capable of inhibiting CD40
PT mediated cell activation - useful to treat conditions characterised
PT by aberrant or unwanted level of CD40 mediated intracellular
PT signalling
PS Example 1. Fig 1A-P. 158pp. English.
CC This 2918 bp cDNA sequence encodes CRAF1 (TRAF-3) and its deletion
CC and alternative splice isoforms (see W27428-37). It is derived
CC from several cDNA species from a Raji B cell library. CRAF1
CC peptides, comprising from 0-4 zinc finger domains, and nucleic
CC acids encoding them, can be used to inhibit CD40 ligand activation
CC of cells that express CD40 on their surface, particularly by
CC introducing the nucleic acid molecule into the cells, useful to
CC treat conditions characterised by an aberrant or unwanted level of
CC CD40 mediated intracellular signalling, such as organ rejection in
CC a subject receiving transplant organs, or a CD40 dependent immune
CC response in a subject receiving gene therapy. The condition may be
CC an allergic response, an autoimmune response, or may be dependent
CC on CD40 ligand-induced activation of epithelial cells, an
CC inflammatory kidney disease, a smooth muscle cell-dependent
CC disease, or a condition associated with Epstein-Barr virus. CRAF1
CC nucleic acids can also be used as probes in diagnostic testing.
CC The gene for CRAF1 is located on human chromosome 14q32.2.
SO Sequence 2918 BP; 768 A; 728 C; 822 G; 600 T;

```

Db	472	ACCGGCCGGCGCCCTGTAGCCGGCGAGCGGACGGACCGCAAGATGAGAAATAG	531
QY	70	gcccaagaagatgataccacttggttaagttccagagcaagttcagaatcaagacttagga	129
Db	532	GCCCAAGAAGATGATCCACTTGGTTAAGGTCCAGAGAGAGTCCAGAAATCCAGACTGGA	591
QY	130	tcagaaacctggtctctgctctcct -gtccctcaactcttcaaggaatgc -gtcctgaca	187
Db	592	TCGAAACCTGGCTCTCGGCTCCTGGCTCCTCACTCTTCAAGATGCCCTGTCTGACGA	651
QY	188	gaagagactcctcttctcctaaatgtagtcagataaagaatgactctcttgcgcgc	247
Db	652	GAAGAGAACTCTCTTCTTCCATAATGAGTCCAGTAAAAAGATGACCTCTCGCGCGC	711
QY	248	tgcagactaacccgcgcgtcaaaagctcacacgtacccgcgcgcgtctggacgcgcattttg	307
Db	712	TGCGACTTAACCCGCGCTTAAGCTCACACTGACCGTAGCTGGAGGCCAGTTTGTG	771
QY	308	tcctctgacaaggagttacaagaaagtttgtgaagacgcttgaggacaagtaagaat	367
Db	772	TCCTGTAAACAAGGAGGTTTACAAAGAAAGTTTGTGAAGACCTGGAGGACAAGTACAAGT	831
QY	368	gtgagaaagtccacactggtgtctgtgagcccggaagagacgcagagtgtggagccgctct	427
Db	832	GTGGAAGTCCACCTGGTGCTGTGAGCCGGAAGACCCAGAGTGTGGACCCGCTACT	891
QY	428	gcgagagctcagatgcygcctctgctgactctctcaagtcacaatgtaacagcgtltcaag	487
Db	892	GCGAGACTGCATGAGGCGCGCTGTGAGCTTCAAGTCCAAATAGTACAGGCTGTAAG	951
QY	488	agagcatcgtttaaagaiaaagtgtttaaagataattgctgcgaagagagaattctcgtctc	547
Db	952	AGACATCATGTTAAAGATMAAGTGTTTAAGATATTGTCGAAGAGAAATCTGTGGCTC	1011
QY	548	ttcagactctttgtccggaatggaagcagaggtgtgtcagagcaagttaatgctgagacat -	606
Db	1012	TTTCAGATCTATTGTCCGAATGGAAGCAAGAGAGTGTGTACAGCATTAAGCTGGGACATC	1071
QY	607	--ccgtgtacatttaaaaaagatttgcattttgaagaacttccatgtgtgcctgact	664
Db	1072	TGCTGTGATTTAAAAATGATTTGACATTTTGAAGACTTCCATGCTGTGCTCCTGACT	1131
QY	665	gtcaagaagaaggtctttagaagaagacttggagacacgcttgagagaagsgtgttaaatcc	724
Db	1132	GCAAGAAAAGGTTTGAAGAAAGACTGGGAAACACAGTGGAGAGGGCTTAATATAC	1191
QY	725	gggaagcacacatgcaagcactgtcaagaatlcaggtttccgatgtatcgcgtctgcagaacacg	784
Db	1192	GGGAAGCACATGACGACCTGCAAGAGTCAAGTTCAGATGATCGCGCTCAGAAACAG	1251
QY	785	aagacacgactgtccctgctgtgtgtgtgtccgtccctcaacaagtgtcagcgtccagatcc	844
Db	1252	AAGACACCGATGTCCCTGGGTGGTGTGCTCCGCTCACAGTCCACAGCTCCAGACTC	1311
QY	845	tcctgagaagagagtttagatgacacactgtcagagtgtgtcgaatgtcccccagcactgtga	904
Db	1312	TCCTGAGAGCGAATTGATGATCACACTTGTCAAGATGTGTCAATGCCCCACGACTGTGA	1371
QY	905	gttttaagcgtatgctgtcgtgttttccaagggaacaaacagcagatcaaggtcccaagag	964
Db	1372	GTTTAAACGCTATGGCTGTGCTTTTCAAGGGGCAAAACAGCATCAAGAGGCCCAAGAG	1431
QY	965	ccaagtcgcgcgtgcagcagcgtcaactcgttgtaaagagtgtgagcaactcgtgtcgaagaag	1024
Db	1432	CCAGTCCGCGGTCCAGACGTCAACTGCTGGAAGGTGTGACCACTGCTCGAANAAGA	1491
QY	1025	aggttccctgttgcagataaagtttagaaaaaaacagagcatatacaagttttgcaca	1084
Db	1492	AGGTTCTTGTTCAGATGAATAAAGTTAGAAAAAACAAGAGCATTAACAAGTTTGACA	1551
QY	1085	atcagatatagctttgaaattgaaattgagagacaaaagaatgtcttcgaataatgt	1144

Dd	1552	ATCAGATNTCTACTTTGAAATTTGAAATTTAGAGACAAAAGGAAATGCTTCGAAATTAATG	1611
Qy	1145	aatccaaatcccttcattctacagagatgatagacagccaaagcagagaacacttaagagac	1204
Dd	1612	AATCCAAAATCTTTCATTTTACGACAGATGATCGAAGCAAGCAAGAAATCTAAGAGAGC	1671
Qy	1205	ttgcacagagatccgagcccttcgagaaacttggaggaagcagacagatgaagaca	1264
Dd	1672	TTGCAAGGAGATCCGGCCTTCCGGCAACTGGAGAGAACGACAGATGAGAGCA	1731
Qy	1265	gcgtgagatccctccgaacccgctgaccagcttgagagacgtgacaaagacgcggygc	1324
Dd	1732	GGGGAGTCCCTCCAGAAACCGGGGTGACCGACTGGAAGCGTGGAAAGAGTGGGGGC	1791
Qy	1335	aafgagctcggaacaaagagccctgcgtctggagctccagctagccgagcagacaatgtctga	1384
Dd	1792	AAGTGGCTCGGAACACAGGCTCTGTGAGTCCCACTGATGCGCGGCAATGACAGATGTGA	1851
Qy	1385	gtgtgcacgacatccgactagccgacatgagcttgcgtcccaagtcctctgagacgcga	1444
Dd	1852	GTGTGCACGACATCCCGCTAGCCGACATGAGACTCGCTTCAGAGTCTCGAGACCCCA	1911
Qy	1445	gtcacatgagatggtcactcttggaaagattcggagactaaagccgacggaagcagagccg	1504
Dd	1912	GCTCAATGAGGTGCTCATCTGGAAGATTCGGCACTTAACGGCGGCAAGCAGAGAGCCG	1971
Qy	1505	tcaatgggaagaccctgtccctcttaagcagaaccccttctaacttgatcttggctata	1564
Dd	1972	TCATGGGGAAGACCCGTGCTCCCTTTACAGCCACCTTTCTACACTGGTACTTGTGTATA	2031
Qy	1555	agatgtgtccagaggtctactctgaacggggaagggatgagggaagggagagacatgtgcg	1624
Dd	2032	AGATGTGTGCCAGGGTCTACTTAACGGGGAGCGGATGGGAAGGGAGCGACTGTGCGC	2091
Qy	1625	tgtttttgtcatcatgcgtggaagaaatgaatgcctcttcctcttgcgcgtttaagaca	1684
Dd	2092	TGTTTTTGTCATCATGCTCGTGGAGATATGATGAGCCCTGTTCCCTTGGCCGTTTAAGAGA	2151
Qy	1685	aatgtaacatcatgtctgaatgatacaggggtccctctcgacgtcaatttggagatgatca	1744
Dd	2152	AAGTACACTCATCTGATGATGATCAAGGGGTCCCTCGACGTCATTTGGGAATCAATCA	2211
Qy	1745	agcccgaccoccaaagagagagtttaagaagaaccaatggagagatgatatgcgctctg	1804
Dd	2212	AGCCGACCCCAACAGACGACGCTTAAAGAACCCACTGAGAGATGAAATTCGCCCTCG	2271
Qy	1805	gctgcacagctcttggcccacaactgctctcagaagaatggagacatatattaagatata	1864
Dd	2272	GCTGCCCAGTTTGTGTGGCCCAACGTCTTGAAATGCGACATATTTAAAGATGATA	2331
Qy	1865	caattttatttaagtgatagtgtgacttgcgacttgcgcgaccccgataaagtatgtg	1924
Dd	2332	CAATTTTATTAAGGTATAGTGGATATCTTCGATCTGCCGATCCCGATTAAGTAGTG	2391
Qy	1925	ggagagtgatattagcagaagagcaactcctcttggggaatttgaacccgtctgtcctcaat	1984
Dd	2392	GGGAGTGGATTTTGAAGAGGCAACCTCTGGGGATTTGAACCGTCTGTCTACT	2451
Qy	1985	gaagtccctgcgctccagaaaaagaccttgtgagacgaggaagcggcgaagagcgaagc	2044
Dd	2452	GAAGTCTCTCGGCTCAAAAAAGCACTGTGAGACCGAAGAGCGGCAAGAGCGGAGCGC	2511
Qy	2045	gtgcgagcgggagagcagacgagagcaaacctgtgcaggttataaataagactagccac	2104
Dd	2512	GTGCGCGGGAGAGGACGACGGGAGACAACTGACAGCTTTTAAATAGACTAGCCAC	2571
Qy	2105	acttcaactctgaagaaattattatctctcaacaagaataatatgtctgtcagagaaggt	2164
Dd	2572	ACTTCACTCAAAATATTTATTCCTTCAACAAGATAATTTCTGTCAAGAGAGGTT	2631
Qy	2165	ttcatctttcttttaagatctagttaatatgaagtgaggaaacatatatgtctcaacaaa	2224
Dd	2632	TTCAATTTCAATTTTAAAGATCTAGTTAATTAAGGTGGAAAAATATATGCTAAACAAA	2691

QY	2225	gaacacgtgttcttctcttcaacttgaaccccaaaaaaacacacacacacacacgt	2284
Db	2692	GAACATGATTTTCTCTCTCTTAACCTGACACCAAAAAAACACACACACACACACGT	2751
QY	2285	ggggatagctgacatgctcagcatglttaagtaaaaggagaattatgaatagta	2339
Db	2752	GGGGATAGCTGACATGTCAGCATGTTAAGTAAAGGACAAATTTATGAATAGTA	2806
RESULT	3		
ID	T31273	standard; DNA; 2359 BP.	
AC	T31273;		
DT	23-OCT-1996	(first entry)	
DE	LMP1 associated protein LMP1 gene.		
KM	LMP1, LMP1 associated protein 1; latent infection membrane protein;		
KW	tumour necrosis factor receptor associated factor; TRAF;		
sig	signal transduction; TNF; TNFR; lymphoblast; tumorigenesis; AIDS;		
OS	Hodgkin's disease; Burkitt's lymphoma; nasopharyngeal carcinoma;		
OS	mononucleosis; Epstein-Barr virus; EBV; gene therapy; ss.		
FN	Homo sapiens.		
FT	Key	Location/Qualifiers	
FT	cds	151..1857	
FT		/tag= a	
PN	MO9620723-A1.		
PD	11-JUL-1996.		
PF	28-DEC-1995; U16980.		
PR	30-DEC-1994; US-367540.		
PA	(BGHM) BRIGHAM & WOMENS HOSPITAL.		
PA	(RESC) UNIV CALIFORNIA.		
PI	Birkenbach M, Kaye KM, Kieff E, Mosialos G, Vanarsdale T;		
PI	Ware C;		
DR	WPE 96-333765/33.		
DR	P-PSDB; W03146.		
PT	Compounds and methods for controlling TRAF-mediated signals - by		
PT	modulating interactions between Epstein Barr virus encoded proteins		
PT	LMP1, LMP1, TNF, TNFR to inhibit lymphoblast growth and		
PT	tumorigenesis.		
PS	Example 1; Page 58-60; 87pp; English.		
CC	A DNA sequence (T31273) codes for a novel B-cell protein (W03146)		
CC	termed LMP1 associated protein 1 or LMP1, which strongly associates		
CC	with the cytoplasmic C-terminal domain (W03148) of Epstein-Barr virus		
CC	(EBV) latent infection membrane protein 1 (LMP1), a domain that is		
CC	stringently required for transformed cell growth. LMP1 is related to		
CC	murine tumour necrosis factor receptor associated factor TRAF2. The		
CC	gene was identified using a yeast 2-hybrid screen. It can be used in		
CC	gene therapy protocols for controlling TRAF-mediated TNF/TNFR signal		
CC	transduction, or for the prodn. of LMP1 polypeptides that inhibit		
CC	LMP1-TRAF interaction and are useful in treating infection and		
CC	controlling cell growth/tumourigenesis associated with LMP1-encoding		
CC	viruses, partic. EBV.		
CC	Sequence 2359 BP; 668 A; 533 C; 628 G; 530 T;		
Query Match	95.7%; Score 2238.8; DB 1; Length 2359;		
Best Local Similarity	99.6%; Pred. No. 0;		
Matches 2276; Conservative	0; Mismatches 2; Indels 6; Gaps		
QY	62	aaaatgagcccaagaagtgatgccaacttgggttaaggtccagagcaggtcagaatcag	121
Db	1	AAAATGAGCCCAAGAAGTGAATGCGACATGGTGAAGTGCCAGAGCAGAGTCAGATCAG	60
QY	122	acctgagatcaaaaactcgtcctcgtgctcct-gctccctactcttctaagatgcgtt	180
Db	61	ACCTTAGATCAAAAACCTGCTCCCTGCGCTCCGCTCCCTACTCTTAAAGATGCTCTT	120
QY	181	cctgaagaagaagaactcctcttctcctaataatggaatgagatcaaaaagatgactcct	240
Db	121	CCTGACGAGAAGGAATCCTCTTTCTTCTTAATAAGATCGATCGATGAAAAGATGGACTCTCT	180
QY	241	ggcgcgcgcagactaacccgcgcgctaaagtgcacactgacgcgacgtctgagacgca	300

D	b	181	GGCGGCGTCAAGACTAAACCGCGCGTAAAGCTGCACACTGACCGGAGTGTGGACGCCA	240
Q	y	301	gttttttcccttgacaagaagggtttacaaggaaagtttvtgaagacgvtgaggaacaag	360
D	b	241	gttttttgcctctgaaacaaagaggtttacaaagaaaattttgtgaaacacgttgagacaaag	300
Q	y	361	tacaagvtgtgaagvtccaccctgtgtgtgtgaagccggaagcagaaccgagvtgagac	420
D	b	301	TACAAgTGTGAAGAGTCCACCTGTGTGTGTGCAGGCCCAACAGACGAGTGTGGGCAC	360
Q	y	421	cgcttcgcgagagctgcatgagcgcgcctgtgaactcttcaagtcaccaaatgtacaagc	480
D	b	361	CGCTTCTCCGAGAGACTGCATGAGGGCGCCTGCTAGCTCTTCAAGTCCAAAATGTACACG	420
Q	y	481	tgtaagagagcatcgtttaaagaatgaagtgvtttaagataattgtctgcagaagagaaat	540
D	b	421	TGTCAAGAGAGACCATCGTTAAAGATTAAGTGTTTAAAGATAATTGCTGCACAGAGAAATT	480
Q	y	541	ctggtcttccagactatttgtgaatgaagaagaggttgtgcagagcagttaatgtgt	600
D	b	481	CTGGCTCTTCAGATCTATTGTCCGAATGAAGACAGAGGTGTGACAGACAGTAAATGCTG	540
Q	y	601	ggaact--gtgtgtgcaatttaaaatgatgtgcattttgaaagacttccatgtgtgct	657
D	b	541	GGACATCTGCTGGTGTCATTTAAAAATGATGTGCCATTTGAAAGAACTTCATGTGTGCT	600
Q	y	658	cctgactgcanaagaagaaggtcttgaggaagaacctgcagaccacgttgaagaagcgtgt	717
D	b	601	CCTGACTGCANAAGAAAGGTCCTTGAGGAAGACCTCGAGACACGTGAGAGAGGCGTGT	660
Q	y	718	aaataccgggaaagccacatagcagccaactgcagaagtcgaagttccgaatgacgcgtcag	777
D	b	661	AAATACCGGGAAAGCCACATGCACACCACTGCAGAAAGCAAGTTCGATGATCCGCTCGAG	720
Q	y	778	aaaccggaagccacagacttccctcgtgtgtgtgttctgtccctccaaagtgagcgtc	837
D	b	721	AAACCGAAGACACCGACTGTCCCTGTGTGTGTGTCTCTGCCCTTCACAGTCAGGCTTC	780
Q	y	838	cagaactccctcgaaggaacgagttgagvtgcacactgtcagagttgttcaatccccacgc	897
D	b	781	CAGACTCTCCGAGAGACGAGTGAAGTGCACACTTGTACAGAGTGTCAATCCCCCAGC	840
Q	y	898	aacgtgtagttttaagcgtatggtcgtgttlttcaaggggacaacccagcagatacaaggcc	957
D	b	841	ACCTGATGTTTAAAGCCGTATGCGTGTGGTGTTCACAGGGAACAACGACAGATCAAGGCC	900
Q	y	958	cacgagcgcagctccgcgcgtgcagcagcgtcaacactcgtgaagagtgtgagcaactcgtc	1017
D	b	901	CACGAGCGCACCTCCGCGGTCAGACACGTCAACCTCTCAAGAGAGGCAACACCTGCTC	960
Q	y	1018	gaaagaagaggttccctcgtgtgcagaatgaagaagtgtgaaaaaaacaagagcatalcaagt	1077
D	b	961	GAAAAGAAAGTTCTCTTGTTGCCAATGAAAGTGTGAAAAAACAAGAGCTTACAAAGT	1020
Q	y	1078	ttgcacaatcagatalgtlaagctttgaatatgaatatgagaacaaaggaaatgtcttga	1137
D	b	1021	TTGCACATCAGATATGTAGCTTTGAATGTGAATGTGAAAGACAAGAAAGTAATGCTTGA	1080
Q	y	1138	ataatgaatccaaaatcccttcatcttaacagcgagvtatagacagccaagcagaactgt	1197
D	b	1081	AATATGAAATCCAAAATCTTTCATTTCACGCGAGTATGACAGCCACAGCAAGCAAGAACTG	1140
Q	y	1198	aagagagcttgcagaagagatccggcccttcggcagaaactgtggaggaagcagaacagctg	1257
D	b	1141	AAGGAGCTTGCAAGAGAGATCCGACCCCTTCGGCAAACTGGAGAGAACACACAGCATG	1200
Q	y	1258	aagagcagcgttgcagatccctcccaagaacccggtgtaccgagcttgaagcgttgcacaagc	1317
D	b	1201	AAGAGCAGCGTGTGAGTCCCTCCAGAAACCGGTGTACCGAGACTGAGAGGCTGACAAAGC	1260
Q	y	1318	gcggaggcaagtgtgtcgtgaacacagacgtgtgtgaagttcccaagctgtagccgcgtacag	1377
D	b	1261	GCGGGCGAAAGTGTCTCGAACACAGGCTGTGTGATCTCCACACTAGCCGGCATATACAG	1320

[illegible]

AC	T30773; -1998	(first entry)	-1 encoding DNA.
DE	CD40 associated protein (CAP)-1		gene therapy;
KM	CD40 associated protein; CAP; agonist;		autoimmune disease; ss.
OS	Homo sapiens.		
FH	Key	Location/Qualifiers	
FT	CDS	137..1768	
FT	/tag= "CAP-1 protein"		
PN	W0616665-A1.		
PD	06-JUN-1996.		
PF	04-DEC-1995:	US5695.	
PR	02-DEC-1994:	US39357.	
PA	(LJOL-) LA JOLLA CANCER RES FOUND.		
DR	Reed JC, Sato T.		
PT	WP1; 96-286818/29.		
PT	P-PEDB; R98833.		
PT	New CD40 associated protein, agonists and antagonists - used to modulate cell proliferation, immune response, apoptosis etc., e.g. for treating cancer or autoimmune disease		
PS	Claim 13; Fig 1; 94PP; English.		
CC	This DNA encodes a CD40 associated protein (CAP)-1. The CAP is a protein that specifically binds to CD40, a cell surface receptor involved in apoptosis. Agonists and antagonists of CAP can increase or decrease the level of GAP expression in a cell and can thereby modulate the function of the cell. Such compounds can be used to treat cancer, CC autoimmune diseases like asthma, hay fever, rheumatoid arthritis and CC immunodeficiency diseases and neurodegeneration. Antibodies that bind specifically to CAP can be used to assay CAP, to detect pathologically altered levels. This nucleic acid can be used to identify related genes and to express CAP for gene therapy.		
CC	Sequence	2240 BP; 637 A; 510 C; 604 G; 489 T;	
SQ			
Query Match	87.1%; Score 2038; DB 1; Length 2240;		
Best Local Similarity	96.2%; Pred. No. 0;		
Matches 2183; Conservative	0; Mismatches 5; Indels 82; Gaps		
OY	76	agaagtgatgcacacttggtaagtcccaagcaggtcagaatcacgacctagatacgaa	135
DB	1	AAGAAGGATGCCACTGGTTAGTGTCAGACGAGTGAATCAAGCTTAGATCATGAA	60
OY	136	accctggcttcgtgctc-t-gctccctaactttctaagatgcgtctctgcagaagaga	194
DB	61	ACCTGGCTCTCTGGCTCGCTCCCTACTCTTTAAGATGCCTGTCTTCCAAGAGAGA	120
OY	195	actctcttctctaataitgagtcgaataaaaagtgcgtctccctggcgctgcagac	254
DB	121	ACTCTCTTCTTAATAATGAGTGCAGTAAAAGATGACTCTCTCGCGCGCTGCAGAC	180
OY	255	taaccgcgcctaaagctcacacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	314
DB	181	TAAACCGCGCGCTAAAGCTCACACGACCGCAGTGTGGAGCGCAATTGTCCTTA	240
OY	315	acaaggaagttacaagaaatttgtagaagccgttgcagcaagttacagtttgagaa	374
DB	241	ACAAGAGAGTTTACAAGAAAGTTTGTGAAGACCCTGGAGGACAATCAAGTGTAGAA	300
OY	375	gtgcacccctgtgtgtgtgtgaagccgaagagacgcgcgcgcgcgcgcgcgcgcgc	434
DB	301	GTCACCTGTGTGTGTGTGCAACCCGGAAGCAGACCGAGTGTGGCACCGTCTCTGCAAG	360
OY	435	cgtcatgtgc	494
DB	361	CTGCATGCGCGCGCTGTGTGTGTGCTCTTCAAGTCCAAATGTACAGCGTGTCAAGAGAGAT	420
OY	495	cgttaaagaataagggtgtttaaggataattgtctgaagagagaattctgtcttcgat	554
DB	421	CGTTAAAGATTAAGTGTTAAGGATTAATGTGCAAGAGAAATTCCTGGCTTTCAGAT	480
OY	555	ctatgtcggaatgaagcagaaggttgttgcagaagcgttaaacgtcggagcat---ctgat	611

Db 481 CTATTGTCGGAATGAAGACAGAGGTTGTGACAGCAGTTAACGCTGGACATCTGCTGCT 540
 Qy 612 gcatltaaaaaatgattgcatltaagaactlcaatgltgctgctgactgcaaga 671
 Db 541 GCATTTAAAAATGATTTGCCATTTTGAAGAACTTCCATGTGTGCTGCTGACTGCAAAA 600
 Qy 672 aaaagtlcttgaaagaagactctgagaaacacgltggaagagcggtgttaataaccggaagc 731
 Db 601 AAAGGCTTGAAGAAAGACCTCGAGAACACAGTGGAGAGGCGTGTAAATACCGGGAAC 660
 Qy 732 caacatgcaagcaactgcaagaatcgaagttccgatgacgctgcaagaacacgaagacac 791
 Db 661 CACATGCAACCACTGCAAGAGTCAAGTTCCGATGATCGGCTGCAAAAACAGAAACAC 720
 Qy 792 gcaatgctccctgctggtggtgltccctgacacgaatgcaagctgcaagactctctgag 851
 Db 721 GCACGTGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
 Qy 852 gacgagttgagtgcaactgtgcaagtgltcaatgccccacgaactgtagtlttaa 911
 Db 781 GAGCG----- 785
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 Db 786 -----AGGGGCAAAACAGCAGATCAAGGCCACAGAGGCCAGCTC 825
 Qy 972 cgcgctgcaagcagctcaactgtgaaagatggaagcaactgctgcaagaagaagtttc 1031
 Db 826 CCCCCGTGACGCTGCAACCTCTGAAAGAGTGAAGCACTGCTGCAAAAGAAAGTTTC 885
 Qy 1032 ctgtgtgcaagatgaaagtgtlaaaaaaaacagaagcacaagaatttgcacacatcaat 1091
 Db 886 CTGTGTGAGATGAAGTGTGAAATGAAACAAAGACATCAAAAGTTTGCACATAGAT 945
 Qy 1092 atgtgcttgaatgaaatgagagacaaagaaatgctcgaaataatgataca 1151
 Db 946 AGTGTGCTTGAATGAAATGAGAGCAAAAGGAAATGCTTGAATGAAATGAAATGAAATG 1005
 Qy 1152 aatcttcttaacagagcagatgagacagcagaagaaactgaagaagctgtgaca 1211
 Db 1006 AATCTTCTTACAGCGAGTATGACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1065
 Qy 1212 ggaagatccgacccctccgagcagaactggaagaggaagcagaacatgaagcagctgga 1271
 Db 1066 GGAAGATCCGCGCTCTCCGCGAGAACTGGAGAGAGAGACAGCATGAAGCAGCTGGA 1125
 Qy 1272 gtccttccagaacgagcgtgacgagctggaagcgtgtgaacaaagcgcgggcaagtgac 1331
 Db 1126 GTCCCTCCAGAACCGCTGACCGAGCTGAGAGCGTGACAAAGAGCGCGGCAAGTGCG 1185
 Qy 1332 tcggaacaaagcctgctgagatgccagctgagcggatgacagatgctgagtgca 1391
 Db 1186 TCGGAACAAAGCCTGCTGAGTCCAGCTGAGCGGCAAGCAATCTGAGTGTGA 1245
 Qy 1392 ggaacatccgacccctccgagcagaactggaagcgtgctgcaagcgtggaagcgcagctaca 1451
 Db 1246 GCACATCCGCGCTGAGCAGATGAGACTGCGCTTCCAGGTCTCTGAGAGACCGCAAGCTGCA 1305
 Qy 1452 tggagtgctcatctggaagatctgcgactacaaagcgcggaagcgaagcgcgtcatggg 1511
 Db 1306 TGGAGTGCTCATCTGGAAGATTCGCGACTACAAAGCGGAGAGAGAGAGCGCTCATGGG 1365
 Qy 1512 gaaagacccctgcttcaagcagccttctacactggttacttggctataaagatggtg 1571
 Db 1366 GAAGACCCCTGCTTACAGCAGCTTCTACACTGTGTTGCTAATAAAGATGAG 1425
 Qy 1572 tgcagaggtctacactggaagcgcggaagcgcggaagcgcggaagcgcggtctgtttt 1631
 Db 1426 TCCCAAGGCTCTACCTGAACGGGAGCGGATGGGAGAGGGAGCACTTGTGCTGTTTT 1485
 Qy 1632 tgtcatcatgctggaagatgagatgctgcttctgctgctgcttgaagcagaagtgac 1691
 Db 1486 TGTCAATCAATGCTGAGAAATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1545

Qy 1692 actatgctgagatgacaggggtctctgacgctatttgggagatgacatcaagccga 1751
 Db 1546 ACTCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1605
 Qy 1752 ccccaacagcagcagcttcaagaagccacatggaagatgaaatcgcctgctgctgccc 1811
 Db 1606 CCCCAACAGCAGCAGCTTCAAGAACCCCACTGAGAGATGATGATGATGATGATGATGAT 1665
 Qy 1812 agtcttctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1871
 Db 1666 AGCTTTTGGGCCAAACTGTTCTGAAATGAGACATATATTAAGATGATGATGATGAT 1725
 Qy 1872 taataagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1931
 Db 1726 TATTAAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1785
 Qy 1932 ggaattagcagaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1991
 Db 1786 GGATTTAGCAGAAAGCACTCCTGAGGAGATTTGAACCGGTCTGCTGCTGAGGTCC 1845
 Qy 1992 tgcgctcagaagaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2051
 Db 1846 TCGCCTCAGAAAGAGACCTTGTGAGAGCAGAGAGCGGCAAGGCGGAGCGGCTGCGG 1905
 Qy 2052 cggagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2111
 Db 1906 CCGGAGAGACCGCGGTGAG-ACACTGACACGTTTATTAATGATGATGATGATGATGAT 1964
 Qy 2112 tctgaagaattatctatccttcaagaag-ataaatgtgctgagagaagtttcatl 2170
 Db 1965 TCTGAAGATATTTATCTTCAACAGCATTAATGCTGCTGAGAGAGTTTTCAT 2024
 Qy 2171 ttcattttaaagatcagtaataatgagtggaagacatataatgctaaacaaagaaca 2230
 Db 2025 TTCATTTTAAAGATCTGATTAATTAATGAGTGAAGAAACATATGCTTAAACAAAGAA 2084
 Qy 2231 tgatttcttcttcaacttgaacacacacacacacacacacacacacacacacacac 2289
 Db 2085 TGATTTTCTCTTAACTTAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 2144
 Qy 2290 tagctgagcagctgacagcagctgtaagtaaaagagagatattgaataagta 2339
 Db 2145 TAGCTGAGACATGTCAGCATGTTAAGTAAAGAGAGATTTAATAATGATGA 2194
 RESULT 5
 ID T88022 standard; cdna to mRNA; 2105 BP.
 AC T88022:
 DT 27-APR-1998 (first entry)
 DE Murine TRAF5 CDNA.
 KW Murine; mouse; TRAF5; tumour necrosis factor; TNF; allergy;
 KW receptor associated factor family; immunisation; treatment;
 KW cell proliferation inhibitor; screening; inhibitor; regulator; ss.
 OS Mus sp.
 FH Key Location/Qualifiers
 FT CDS 188..1864
 FT /*tag= a
 FT /product= TRAF_5
 PD WO9738099-A1.
 PD 16-OCT-1997.
 PF 10-APR-1997; J01236.
 PR 25-DEC-1996; JP-353847.
 PR 11-APR-1996; JP-113035.
 PA (MOCH) MOCHIDA PHARM CO LTD.
 PI Inoue T;
 DR WPT: 97-512716/47.
 DR P-PSDB: W27609.
 PT TRAF5, protein of tumour necrosis factor receptor associated factor
 PT family - useful in immunisation, to treat allergies and as cell
 PT proliferation inhibitor
 PS Claim 12; Pages 41-44; 80pp; Japanese.

CC The present sequence encodes murine TRAF5 a protein of the tumour
CC necrosis factor (TNF) receptor associated factor family. TRAF5
CC products can be used in immunisation, to treat allergies and as
CC cell proliferation inhibitors. They can also be used to screen for
CC TRAF5 inhibitors or regulators. 530 C; 578 G; 457 T;
SQ Sequence 2105 BP; 540 A; 530 C; 578 G; 457 T;

Query Match 15.3%; Score 358; DB 1; Length 2105;
Best Local Similarity 55.0%; Pred. No. 8.1e-88;
Matches 876; Conservative 0; Mismatches 695; Indels 21; Gaps 8;

QY 327 caaagaaagatttgaagaccgtggaagacaagatgtagaagtgccacctgt 386
DB CGAGTACAGATTGTTGAGCAGCTGGAAGACGCTCAATATGCTTGCACCTCCGT 339
QY 387 gctgtgacccgaagacaagcagatgtgtggaacccctctgacagagtgatgagc 446
DB 340 GCTTCAACACCCGACCAACGCGCTGCGGACCCCTTCTGCACAGTCCGCTC 399
QY 447 cctgtgagct---ctcaagtcacaatgtacagcgtgtcaagagagcattgtaaga 503
DB 400 TCTGAAGATTAATGATCGGTGCGGATCTGCCGTTAGACAGAGAGTCAAGCTCA 459
QY 504 taagtgattaaagataatgtctgcaagagagaatcttgcctctcagatctatgtcg 563
DB 460 GGGAGTGTTCAGAGACACTGCTGCAAAAGAGTTCATTTACAGTCTACT--G 516
QY 564 gaatgaagacagaggtgtgtgacagacagtaatgtcgtgagacatctgtcatlaaaaa 623
DB 517 CAAAAACCCCCCGGTGCAATCCAGATTAATCTGGAGCATTCAGAGACCACTTCA 576
QY 624 tgattgcatlittgaagaattccatgtgtgtcctgtacgtcaagaagaagctttag 683
DB 577 GCACGTCTCTTCCAAAGCCGCTGCTGCCCTTAACGAGAGCTGCGGGAACCAATGCTCCG 636
QY 684 gaaagccctgacagacagtgagagaggtgttaataacagagagacacatgacac 743
DB 637 GAAAGAGTGAAGAGACCTAGAGCCGATACCTCCGCTTCCAGAGAGAAAGTCCCTTA 696
QY 744 ctgcaagagtcaggttcgcagatgcgcgtcgcagaaacacagagacacgcagctgcctg 803
DB 697 CTGCAAAAGGAGATAGTGTGTGACCAACCTGAGAGATCATGAGAGAAATCGTCTCCTCG 756
QY 804 cgtgtgtgtgtcctgcccctcaagtgacagcgtccagactctcctgaagagcgagttgag 863
DB 757 GTACCCAGTGTCTTGTGCCAACAGGTG--TGTGACAGACTATTCCAAAGACTAGGGTGA 813
QY 864 tgacacactgtcagagtggtgtcaatgtcccccagcacctgtagtttaagcgtatgctg 923
DB 814 TGAACACCTTACTGTATGTCTGAGGCTGAGCAAGACTGTCCCTTTAAGCACTATGGCTG 873
QY 924 cgtlittcaggggacaacacagcagatcaaggtccacagagcagctcgcgtgtcagca 983
DB 874 CACTGTAAAGGTAAGGGGGGAATCTGTGAGCATAGACGGGACACCTTCGACGAGCA 933
QY 984 cgtcaacctgtcgaagagtgagagcaactcgtctgcaaaaagaagtttccctgtgtcgaa 1043
DB 934 CATGCTTCTGTGTTTAAAGAGAACTCAACTTAAGAACGGGATCTCTGATTATATCA 993
QY 1044 tgaagagtgtaaaaaaacaagagcatataaagtttgacaatcagatgtagtttga 1103
DB 994 GAGTCTGAAACAGAAAGAAAGATCCAGACTGCGAGAAACCGTTGAAGAGTTGCA 1053
QY 1104 aattgaatitgagagacaagaagaatgtctgcaataatgaatccaaatcccttcatc 1163
DB 1054 AAAGAGACTTAAGCAGTTCAACAGATGTTTGCAAAATGGAATCTTCCCTCAAAATGT 1113
QY 1164 acagcagtgatagacagccagcagagagaactaagaagagtttcaagaagagatcggcc 1223
DB 1114 CCAG---GCTTCAACAGGTACACAGGACAACTGCTTGGTGAAGCGCAGGTGCGCA 1170
QY 1224 ctccgcagagactgagagagagacagatgaagagcagctgtgagtcctccacaga 1283

DB 1171 GCTGTACA-AATAGTTACACAGCCCACTGCACTTGAATCTAGGCTTTGGT-GGAT 1228
QY 1284 ccgctgacccagctggaagcgtgtgacaagagcgtggaagtgctcgaacaagg 1343
DB 1229 GCGGTGACAGCGTGAACAGAGATCACCCAGCTGAGACAGTAC-CAGAGATTAGT 1287
QY 1344 cctgtgtgagtcaccagctcgaacccgcatgacacatgtgtgtgtgtgacagcaccct 1403
DB 1288 TCTTTTAAGGGGGGAGACCAACAGCACAGCACACTTAATATCCAAAGACAGCT 1347
QY 1404 agccagacatgacacgtgtgtccagctcgtgagacccagcagcacaatgtgtgcat 1463
DB 1348 GAATAGAACAGAGACCGCTTTAAGCACTGAGAGGCGCCGCTACATGAGCAAGCTCAT 1407
QY 1464 ctggaagattcgcagactacaagcgtggaagcgtgtcatatgtgtggaagacctgtc 1523
DB 1408 CTGGAAGGTGACAGATATACAGGTTGAGAGAGAGGAGCGGTGAGAGGCGACAGTGTG 1467
QY 1524 ccttaacagcagcctttctacactgtgtactgtgtgtatgaatgtgtgtgcaaggtcta 1583
DB 1468 GCTTTCAGCCAGCCTTCTACACAGCCGCTGCGCTACCGGCTCTGTGCGAGGCGTA 1527
QY 1584 cctgaacggtgacggtatggtggaagagcagcactgtgtgtgtgtgtgtgtgtgtgt 1643
DB 1528 CTTGAAGGGGAGGCGGTGGGGAAGGAAAGCAGCACTGTCCCTGACTTGTGTGTATCG 1587
QY 1644 tggagaataatgtccctgtctcctgtcctgtgtgtgtgtgtgtgtgtgtgtgtgt 1703
DB 1588 CGTGTAGTGTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1647
QY 1704 ggtacaggtgtctctcgtcagcgtcattgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1763
DB 1648 GACACAGAGCGGCAAGAGAAACATATGTGTGAGACCTTCAAGAGTGAACCCAGAGAG 1707
QY 1764 cagcttcaagaagccacatgtgagagatgaataatgcctctgtgtgtgtgtgtgtgtgt 1823
DB 1708 CAGCTTCAAAAGGCAAGAGGCGGAGATGAACTTCTGCTGCTGCTGCTGCTGCTGCTG 1767
QY 1824 ccaactgtgtcaga-----aaatggtgacatatataagaatgtatattatata 1877
DB 1768 GACCTCTACTGTGAGAACTCCAGAGAACCTTACTTAAGAGCAGACACTGTCTTGA 1827
QY 1878 agtcatagtgatcactcgtgacatgcgcagatc 1909
DB 1828 AGTGCGCGTGAATTAAGTACTGAGTGTGAGATC 1859

RESULT 6
T87039
ID T87039 standard; cDNA to mRNA; 2254 BP.
AC T87039:
DT 18-MAR-1998 (first entry)
DE DNA encoding murine TRAF5, a novel TNF receptor factor family protein.
KW TRAF5; tumour necrosis factor receptor; TNF;
KW TNF signal transducer system; ss.
OS Murine sp.
FH Key : Location/Qualifiers
FT CDS 323..1999
FT /tag a
FT
FT
FT WO9731110-A1.
PD 28-AUG-1997.
PF 24-FEB-1997; J00512.
PR 22-FEB-1996; JP-034674.
PA (SUME) SUMITOMO ELECTRIC IND CO.
PI Nakano H, Nakata M, Okumura K, Yagita H;
DR P-PSDB; W29257.
DR P-PSDB; W29257.
PT Tumour necrosis factor receptor associated factor family protein.
PT TRAF5 - useful to study signal transduction in tumour necrosis
PT factor receptor family
PS Claim 2: Pages 44-46; 69pp; Japanese.
The present sequence encodes a novel protein, designated TRAF5, which is

PA (MOCH) MOCHIDA PHARM CO LTD.
 PR Inoue J;
 DR WPI: 97-512716/47.
 DR P-PSDB: W27610.
 PR TRAF5, protein of tumour necrosis factor receptor associated factor
 PR family - useful in immunisation, to treat allergies and as cell
 PR proliferation inhibitor
 PR Claim 13: Pages 52-57; 80pp; Japanese.
 CC The present sequence encodes human TRAF5 a protein of the tumour
 CC necrosis factor (TNF) receptor associated factor family. TRAF5
 CC products can be used in immunisation, to treat allergies and as
 CC cell proliferation inhibitors. They can also be used to screen for
 CC TRAF5 inhibitors or regulators.
 SQ Sequence 3993 BP; 1198 A; 798 C; 865 G; 1132 T;

Query Match 13.4%; Score 313.8; DB 1; Length 3993;
 Best Local Similarity 53.3%; Pred. No. 1.3e-75;
 Matches 853; Conservative 0; Mismatches 722; Indels 26; Gaps 8;

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149 actaccagtttggagcgggtggagagccgctacaaatgtgcttctgcactcgtgc 208
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QY tctgcaagcccgagacagagctgtgtgacacgcttctgcaagagctgacgtgcgc 448
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QY 506 aggttttaagagataatctgcaagagagaaatctgctcttcagactatctgtgcga 565
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DB 389 atgcctcctgagatgatatgc---caagcttatctggcggcggaacacacacacacac 445
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QY 626 attgcaattctgaagaacttccatctgtgtcctgtacgtcaagaagaagaagctgtgaaga 685
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DB 446 actgcttattttacactgctgacgtgttctaatgagaaagtcggcgagccacacacacac 505
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QY 686 aagactctgagacacacacacacacacacacacacacacacacacacacacacacac 745
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DB 506 aagactctgagacacacacacacacacacacacacacacacacacacacacacacac 565
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    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 866 caccactgtcagaagtggtgcaatgcccccaagcaccctgtgttaagcctatgtgtgcg 925
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 683 aacacctgtgctgtatgtccttgagactgagcaaaagactgctttttttagcactatgtgtgcg 742
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 926 ttttccaggggagacacacacacacacacacacacacacacacacacacacacacacac 985
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 743 ctgttaacgagatataacgagagacacacacacacacacacacacacacacacacacac 802
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 986 tcaacctgtcgaagagtgagacacacacacacacacacacacacacacacacacacac 1045
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 803 tccggttggcttttgaagaaagtgctcaatttagaagaaacagattttctgacttaagacaa 862
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1046 aaaaagtgagaaaaaaacacacacacacacacacacacacacacacacacacacacac 1105
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 863 gccctagaaacagaaagaaatgaaatccacacacacacacacacacacacacacacacac 922
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1106 ttgaaattgagagacaaagaaatgcttcgaataatgatacccaaatccttattac 1165
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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DB 923 aggaattcagacagatttgacacagttgttgccaaaaaattggaagcttccccaacacac 982
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1166 agcgagtgatagacagcccaagagaaactgaagagctgtcaagaagatccggcct 1225
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 983 ac---gtttttccacagctacattgacacacacacacacacacacacacacacacacac 1039
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1226 tccggcagacacacacacacacacacacacacacacacacacacacacacacacacac 1285
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1040 ttttaccacacacacacacacacacacacacacacacacacacacacacacacacac 1095
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1286 gctgtacacacacacacacacacacacacacacacacacacacacacacacacacacac 1344
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1096 gcagttgagatagacagacacacacacacacacacacacacacacacacacacacacac 1155
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1345 ctgctgagacacacacacacacacacacacacacacacacacacacacacacacacac 1404
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1156 gtttttagaagagacacacacacacacacacacacacacacacacacacacacacac 1215
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1405 gccgacatgacacacacacacacacacacacacacacacacacacacacacacacacac 1464
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1216 acttaaaatgaaagacagatttaaacctgtgagagcttctgtatratgaaagctcatt 1275
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1465 tggagatttcgacacacacacacacacacacacacacacacacacacacacacacacacac 1524
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1276 tggagatttcgacacacacacacacacacacacacacacacacacacacacacacacacac 1335
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1525 cttaacacacacacacacacacacacacacacacacacacacacacacacacacacac 1584
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1336 atcttcacacacacacacacacacacacacacacacacacacacacacacacacacac 1395
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1585 ctgaacacacacacacacacacacacacacacacacacacacacacacacacacacac 1644
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1396 ctgaattggagagagagagagagagagagagagagagagagagagagagagagagag 1455
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1645 ggaagatatgacacacacacacacacacacacacacacacacacacacacacacacacac 1704
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1456 ggagagatttgacacacacacacacacacacacacacacacacacacacacacacacacac 1515
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1705 gatcagagagctcctcagacacacacacacacacacacacacacacacacacacacacac 1764
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1516 gacacagagagagagagagagagagagagagagagagagagagagagagagagagag 1572
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1765 agctcaagagacacacacacacacacacacacacacacacacacacacacacacacac 1824
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1573 accttttaaaagacacacacacacacacacacacacacacacacacacacacacacacac 1632
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1825 caaacctgttctagaacacacacacacacacacacacacacacacacacacacacacacac 1878
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1633 catctgcttttgagagacacacacacacacacacacacacacacacacacacacacacac 1692
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1879 gtcataagtgatactcgcagatcgcagacacacacacacacacacacacacacacacac 1919
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1693 gtagccgtgagacacacacacacacacacacacacacacacacacacacacacacacac 1733
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 9

T31274
 ID T31274 standard; DNA: 2380 BP.

AC T31274;
 DT 23-OCT-1996 (first entry)
 DE Epstein-Barr induced protein EB16 gene.
 KW EB16; Epstein-Barr induced protein EB16 gene.
 KW LMP1 associated protein 1; latent infection membrane protein;
 KW tumour necrosis factor receptor associated factor; TRAF;
 KW signal transduction; TNF; TNFR; lymphoblast; tumorigenesis; AIDS;
 KW Hodgkin's disease; Burkitt's lymphoma; nasopharyngeal carcinoma;
 KW mononucleosis; Epstein-Barr virus; EBV; gene therapy; ss.
 OS Homo sapiens.
 FH key Location/Qualifiers
 FT cds 76..1326
 FT /*tag- a
 FN W09620723-A1.

PD 11-JUL-1996.
PE 28-DEC-1995: U16980.
PR 30-DEC-1994: US-367540.
PA (BCHM) BRIGHAM & WOMENS HOSPITAL.
PA (REGC) UNIV CALIFORNIA.
PI Birkenbach M, Kaye KM, Kieff E, Mosialos G, Vannarsdale T;
PI Ware C;
PI WPT: 96-333765/33.
DR P-PSDB: W03147.
DR Compounds and methods for controlling TRAF-mediated signals - by
PT PT modulating interactions between Epstein Barr virus encoded proteins
PT LMPL, LAP1, TNF, TNFR to inhibit lymphoblast growth and
PT tumorigenesis.
PT
PS Example 1: Page 61-63; 87pp; English.
PS A DNA sequence (731274) codes for a novel B-cell protein (W03147)
CC induced by Epstein-Barr virus (EBV) infection, termed
CC Epstein-Barr induced protein 6 or EBi6. The protein appears to be
CC the human homologue of murine tumour necrosis factor receptor
CC (TNFR) associated factor TRAF1. The gene can be used in gene
CC therapy protocols for controlling TRAF-mediated TNF/TNFR signal
CC transduction, or for the production of Ebi6 polypeptides that inhibit
CC LMPI-TRAF interaction for use in treating infection and controlling
CC cell growth/tumourigenesis associated with LMPI-encoding viruses,
CC partic. EBV.
SQ Sequence 2380 BP; 544 A; 710 C; 682 G; 444 T;

Query Match	6.6%	Score 155.2	DB 1	Length 2380
Best Local Similarity	57.8%	Pred No. 1.9e-32		
Matches 318	Conservative	0	Mismatches 223	Indels 9
				Gaps 2

QY 1349 ttgagttcccaagctgagccgcatgaccaatgtcgtgtgtgcacgacatccgcctagccg 1408

Db 770 TGGAGCAGAGGCTGTGGAGCTTCAGCAGACCTGGCCAGAAAGACCAGGCCCTGGCA 829

QY 1409 acatgacctggcgcttcaggtcctgtagaccgcagctacaatggagtgctcatctgga 1468

Db 830 AGCTGACAGAGCTTGGCGCTCATGAGAGAGGCCCTCCTTCGATGGCACCTTTCCTGTGA 889

QY 1469 agattcgcgactacaagcgcgcgaagcagcagcgcgcgtcatggggaaagacccctgtccctt 1528

Db 890 AGATCACCATGTCAACAGGGCGGTGCCATGATCGGCCCTGTGGCAGGACCGTCAGCCCT 949

QY 1529 acagccagccttctacactggttacttgcgtataagatgtgtgcagaggtctaacctga 1588

Db 950 TCTCCCGAGCCTTCTACACTGCCAGTATGGCTACAAGTTGTGCTGGGGCTGTACC TGA 1009

QY 1589 acggggacgggatggggaagggacgcaccttgcgtctgttttttcacatcatgcgtgag 1648

1010 ATGGAGATGGCACTGGAAAGAGAACCCATCTGTGCGCTCTTCATCGTGATCATGAGAGGGG 1069

Qy 1649 aatatgatgcctctgcttctcttgccgtttaagcagaagaagtgcacccatgctgatgtatc 1708

Db 1070 AGTATGATGCCCTGCTGCCCGTGGCCCTTCCGGAACAAGGTACCTTCATGCTGCTGGACC 1129

QY 1709 aggggtcctctgcagtcatttgtagatgtcatltaagcccgaccccaacagcagcgt 1768

Db 1130 A---GACACACCGTGAGCAGCCATTGACGCCCTTCCGGCCGTACCACTAGCTCAGCGTCT 1186

QY 1769 tcaagaagcccaactgtgagagatgtaataatcgccctctgtgctgcccaagtcctttgvgcccaaa 1828

Db 1187 TCCAGAGGCCCCAGAGTGAAACCAACGTGGCCAGTGGATGCCCACTCTTCCCCCTCA 1246

1829 ctgttct-----agaaaatggygacatatatttaaagatgatcacatcttatttaaagtca 1882

Db 1247 GCAACTGCAGTACCCAGACGCGCTACGTGAAGGACGACACAAATGTTCCCAAGTCCA 1306

Qy 1883 tagtgatac 1892

Db 1307 TTGTGAGAC 1316

RESULT 10

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ID T12262
AC T12262 standard; cDNA; 2121 BP.
DT 09-APR-1996 (first entry)
DE Mouse TRAF2 cDNA.
KW TRAF2; tumour necrosis factor receptor associated factor 2;
   TNF; CD40; ss.
OS Mus musculus.
FH Key location/Qualifiers
FT cds 48..1553
   /*tag= a
PN W09533051-A1.
PD 07-DEC-1995.
PE 25-MAY-1995; U06639.
PR 27-MAY-1994; US-250858.
   28-OCT-1994; US-331394.
PR 22-MAY-1995; US-446915.
   (GETH ) GENENTECH INC.
PA Goeddel DV, Rothe M,
DR WPI; 96-049310/05.
DR P-PDB; R90578.
PT Tumour necrosis factor (TNF) receptor-associated factors - involved
   in mediation of biological activities of TNF and CD40 ligands
PS Example 3; Page 73-74; 116pp; English.
CC A cDNA clone (T12262) coding for tumour necrosis factor receptor
   associated factor 2 (TRAF2) (R90578) was isolated using a yeast
   two-hybrid system to assay for proteins that associate with the
   intracellular domain (ID) of tumour necrosis factor receptor type 2
   (TNF-R2). The cDNA is used for prodn. of recombinant TRAF2, a new
   factor capable of specific association with TNF-R2 ID and CD40.
SQ Sequence 2121 BP; 506 A; 560 C; 616 G; 439 T;

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Query Match 6.5%; Score 153; DB 1; Length 2121;

Best Local Similarity 57.9%; Pred. No. 7.1e-32;
Matches 311; Conservative 0; Mismatches 220; Indels 6; Gaps 2.

Ov 1356 ccaacttaacccgcataaaccaagatgctgaagtgtgcacgacacccgcctagccgcacatgga 1415

Db 1004 CAAGTGCACACGCTGGAGAGAGGCATCGGCTCAAGGACCTGGCCATGGCTGACCTGGA 1063

1416 cctagcccttcacagctcctgagacccgacgctacatgtagtgcctcatctggaagattcg 1475

Db 1064 GCACAGGTCCTCCAGTTGGAAGTATCCACCTATGATGGGCTTTCATCTGGAAGATCTC 1123

1476 cgaactacaagcgcgcgaagcagagccgcgtcatggggaagaccctgtcccttacaagcca 1535

Db 1124 TGACTTCACCCAGAAAGCTCAGGAAGCCCTAGCTGGCCCGACACACAGCTATCTTCTCCCC 1183

1536 qccttctacactggttactttggctataagatgtgtgcccaggtctacctgaacggga 1595

Db 1184 AGCCTTCTACACACAGCATATGGCTACAGATGTGCTACGAGTCTACTTGAATGGCGA 1243

QY 1596 cgggatgagggaagggacgcactgtcgcgltttttgtcatcatgctgtgagaatatga 1655

Db 1244 CCGCACTGGGCGGGGAATCATCTGTCTCTCTTCTTCTGTTGATGAAGGCCCAATGA 1303

1656 tggcctgcttccttgccggttaagcagaagtgcactcatgctgatgtgatcagggtc 1715

Db 1304 TGCCTCTTGCAGTGGCCTTTATCAGAGGTACATTGATGTTGCTGGACCATAACAA 1363

1716 ctctcgacgtcatttgggagatgcatccaagcccgaccccaacagcagcgttcaaga 1775

Db 1364 C---CGGAGCATGTGATCGACGCATTCAAGCCGATGTAACCTGCTCTCTTCCAGAG 1420

QY 1776 gccacatgagagatgatataatgcctctgctgccagctctttgtgtgcccaactgttct 1835

Db 1421 GCCTGTAGTGCATGAACTGCCAGTGGCTGCCCCCTCTTCTGCCCTGTGTCCAAGAT 1480

QY 1836 aga--aatgagacatatattaagaatgatcaaatTTTtattttaagtcatagtgga 1889

Db 1481 GGAGGCCAGAA TTCCTA GTGCGGGATGATCGATCTTCATCAAGCTATTGTGGA 1537

RESULT 10

RESULT 11
ID T12261 standard; cDNA; 2088 BP.
AC T12261; 1996 (first entry)
DT 09-APR-1996
DE Mouse TRAF1 cDNA.
KW TRAF1; tumour necrosis factor receptor associated factor 1;
NM TRAF1; CD40; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT cds 227..1456 /*tag= a
FT PN W09533051-A1.
FT PD 07-DEC-1995.
FT PE 25-MAY-1995; U06639.
PR 27-MAY-1994; US-250858.
PR 28-OCT-1994; US-31394.
PR 22-MAY-1995; US-446915.
(GETH) GENENTECH INC.
Goeddel DV, Rothe M;
WPI: 96-049310/05.
DR P-FSDB; R80577.
DR PT Tumour necrosis factor (TNF) receptor-associated factors - involved
PT in mediation of biological activities of TNF and CD40 ligands
PS Example 2: Page 69-71; 116pp; English.
CC A cDNA clone (T12261) coding for tumour necrosis factor receptor
CC associated factor 1 (TRAF1) (R90577) was isolated from a cDNA
CC library pred. from the murine interleukin-2-dependent cytotoxic T-cell
CC line C6, using probes based on isolated peptides of TRAF1. The cDNA
CC is used for prodn. of recombinant TRAF1, a new factor capable of
CC specific association with the intracellular domain of the type 2 TNF
CC receptor and CD40.
SQ Sequence 2088 BP; 535 A; 575 C; 561 G; 417 T;

Query Match 6.0%; Score 140.2; DB 1; Length 2088;
Best Local Similarity 56.9%; Pred. No. 2,2e-28;
Matches 300; Conservative 0; Mismatches 216; Indels 9; Gaps 2;

QY 1373 accagagctgagtgatgacagacatccgctacgacatgagctggcttcacgttc 1432
DB 924 AGCAAAACCTGGCTCAAAAAGACAGAGCTCTGGCAAGCTTGAGCAGACTGCGACTCA 983
QY 1433 tggagacggccgctacatgagtgatctatctgagaggttcggcactcaagcgcgga 1492
DB 984 TGGAGGAGGACCTTTGATGCTACTTCTCTGGAAGATCAACCAATGTCACCAACCGGT 1043
QY 1493 agcagagagccgctcatgaggaagaccctgccttaccagcagcctttctacactggtt 1552
DB 1044 GCCAGAGAGCTGTGTGGCCGCGACTGTAGCCTCTTCTCTCAGCTTCTTACACTGCA 1103
QY 1553 accttgcctataagatgtgtgacagaggtctacactgaacgggagcggaagggga 1612
DB 1104 AGTATGAGTACAAAGTTGTGCTGCGCTGTACTGTAACGGGATGGCTCAGGGAAGAA 1163
QY 1613 cgcacttgcgtgttttttttcacatcagcggtgagaaatagatgacctgcttcctg 1672
DB 1164 CCCACCTGCTCTTCACTGATCATATAGAGGAAATACATGCTCTGCTGCTGCTGCTG 1223
QY 1673 cgttaagagagaagtgaacatcctgcatgatgacagaggttcctctgacgttcattg 1732
DB 1224 CTTTCAGGAAACAGTCACTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTT 1280
QY 1733 gagatgcatcaagccgagcccaacagacagacagcttcaagaagccacatggagatga 1792
DB 1281 TTGATGCGCTTCGGGCTGACCTGAGCTAGCTCCTTCACAGGGGCCACAGAGAGAACCA 1340
QY 1793 atatgcctctgtgctgacagcttctgtgtgcccacactgtctt-----agaaatggga 1846
DB 1341 AGGTGGCCCGCGCTGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1400
QY 1847 catataataagatgatacaattttatataaagatcatagtgtact 1893

DB 1401 CCTACGTCAAGATGACACAAATGTTCTCAATGATGCTGCGACT 1447

RESULT 12
ID T86169 standard; DNA; 2004 BP.
AC T86169;
DT 03-DEC-1997 (first entry)
DE Human CAR1 nucleotide sequence.
KW Human, CAR1; Lasp1, MLN 64; MLN 51; hds3; mds2; breast carcinoma cell;
KW Cys-rich region; RING finger domain; CAR motif; TRAF domain;
OS Homo sapiens.
FH Key Location/Qualifiers
FT misc-signal 78..88
FT FT /*tag= a
FT FT /standard_name= kozak_sequence
FT FT poly_a_signal 1975..1980
FT FT /*tag= b
FT FT misc-feature 227..228
FT FT /*tag= c
FT FT /note= "Potential splice site"
FT FT misc-feature 279..280
FT FT /*tag= d
FT FT /note= "Potential splice site"
FT FT misc-feature 385..386
FT FT /*tag= e
FT FT /note= "Potential splice site"
FT FT misc-feature 546..547
FT FT /*tag= f
FT FT /note= "Potential splice site"
FT FT misc-feature 708..709
FT FT /*tag= g
FT FT /note= "Potential splice site"
FT FT misc-feature 858..859
FT FT /*tag= h
FT FT /note= "Potential splice site"
PN W09706256-A2.
PD 20-FEB-1997.
PE 31-JUL-1996; U12500.
PR 09-AUG-1995; US-002183.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PA (CNRS) CENT NAT RECH SCI
PA (INRM) INST NAT SANTE & RECH MEDICALE.
PA (UYPA) UNIV PASTEUR LOUIS.
DR Basset P, Byrne J, Rio M, Tomasello C;
DR P-PDB; W25766.
DR PT Genes amplified and over-expressed in breast carcinoma - located on
PT chromosome 17 q11-q21.3 or 6 q22-q23, useful in breast cancer
PT prognosis and as leukemia markers
PS Claim 1; Fig 6; 197pp; English.
CC This sequence encodes human CAR1 and is deposited as ATCC 97610. The
CC CAR1 polypeptide is localised in the nucleus of breast carcinoma cells
CC and has 3 structural domains. A Cys-rich region is located at the
CC N-terminal of the protein. This region which corresponds to an unusual
CC RING finger domain and is probably involved in protein-protein binding.
CC A second Cys-rich region is located in the core of the protein and
CC constitutes three repeats of an HC3HC3 consensus motif. This domain is
CC possibly involved in nucleic acid or protein-protein binding and has
CC been designated the CAR1 motif. The C-terminal part of the CAR1
CC protein corresponds to a TRAF domain known to be involved in protein-
CC protein interactions. CAR1 may be involved in TNF-related cytokine
CC signal transduction during breast cancer progression. The CAR1 gene
CC is useful as a prognostic marker for breast cancer.
SQ Sequence 2004 BP; 393 A; 591 C; 593 G; 427 T;

Query Match 3.8%; Score 90; DB 1; Length 2004;
Best Local Similarity 56.8%; Pred. No. 1.1e-14;
Matches 193; Conservative 0; Mismatches 135; Indels 12; Gaps 1;

CC transcription. Stat6c is a dominant negative regulator of gene
 CC transcription.
 SO Sequence 17425 BP; 3991 A; 4519 C; 4691 G; 4220 T;

Query Match 1.8%; Score 42.4; DB 1; Length 17425;
 Best Local Similarity 60.3%; Pred. No. 0.35;
 Matches 70; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 54 agatgaggaataatgagcccaagaagtatgccacttggttaagtcacagagcagcgtc 113
 DB 121179 AGATGAGGAATAATGAGCCCAAGAGTATGCCACTTGTTAAGTCACAGAGCAGCAGTGA 12120
 QY 114 agaatgagccttagatgagcaaacctgctccgtcctcgtccctcctactcttca 169
 DB 121119 AGAAGGACAGCTAGATTTAAACCCAGGCACTTGTGCGCTTGAGCCCTTAACTA 12064

SULT 15
 119
 1D V13119 standard; DNA; 1893 BP.
 AC V13119;

DE 11-JUN-1998 (first entry)
 DE Synthetic B. thuringiensis truncated crystal protein 9C (cry9C) DNA.
 KM Chimeric gene: plant cell transformation;
 KM insecticidal crystal protein; ICP; cry9C;
 KM AT-rich sequence expression; crystal protein 9C; ds.
 OS Bacillus thuringiensis.
 OS Synthetic.

FT Key Location/Qualifiers
 FT 9.1886
 FT /*tag-a
 FT /product- cry9C-(truncated)

PM WO9749814-A1.
 PM 31-DEC-1997.
 PM 30-MAY-1997; E02832.
 PR 21-JUN-1996; US-667731.
 PA (PLB2) PLANT GENETIC SYSTEMS NV.
 PI Cornelissen M, Gosselle V, Meulewaeter F, Soetaert P,
 PI Van Aartsen R;
 PI WPI; 98-077177/07.

DR Chimeric gene providing high level expression of AT-rich sequences
 PT in plants, useful for expressing insecticidal crystal proteins -
 PT comprises promoter recognised by polymerase other than RNA
 PT polymerase II which generates uncapped mRNA including two viral
 PT translation enhancing sequences
 Example 1: Pages 88-89; 108pp; English.
 CC The present sequence was used in the preparation of a novel
 CC chimeric gene, comprising: (a) promoter recognised by a
 CC DNA-dependent RNA polymerase other than eukaryotic RNA polymerase
 CC II; (b) DNA sequence encoding a chimeric RNA comprising 3' and 5'
 CC untranslated regions (UTR), plus an AU-rich heterologous coding
 CC sequence; and optionally (c) terminator recognised by the same
 CC polymerase as the promoter. The chimeric RNA is uncapped,
 CC translated in plant cell cytoplasm to form a protein and includes
 CC two translation-enhancing sequences (TES) derived from the 5' and
 CC 3' regions of (sub)genomic RNA of a positive stranded RNA plant
 CC virus, located in corresponding 5' and 3' regions.

CC The chimeric gene can be used to transform plant cells which are
 CC grown into plants that express the protein, specifically a Bacillus
 CC thuringiensis insecticidal crystal protein (ICP), but more
 CC generally any protein that improves, nutritional value, imparts
 CC resistance to herbicides, pathogens or inhibits proteases,
 CC amylases or RNases. TES provide efficient cap and polyadenylation
 CC independent translation of RNA transcripts to give high protein
 CC yields, while the use of a polymerase other than polymerase II
 CC generates large amounts of uncapped/non-polyadenylated RNA, whereas
 CC in current methods high yield expression of AT-rich genes is
 CC difficult to achieve.
 CC Sequence 1893 BP; 389 A; 601 C; 539 G; 284 T;

Query Match

1.8%; Score 41.4; DB 1; Length 1893;

Best Local Similarity 48.5%; Pred. No. 0.19;
 Matches 114; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

QY 1209 caagagatcggccctccgcaagaactggaggaagcagacagatgaagcagcgt 1268
 DB 323 CAACGCTGTAACAGCGCAGCCTCAGAACTGGCTGGCCGACCCCAACGACCCGCAACCT 382
 QY 1269 ggaagtcctccagaaaccggtgacgagctgagagcgctggaagaagcggggaagt 1328
 DB 383 GAGCGTGTGAAGGCCCACTTCATCGCCCTGGAACCTGGAACCTGTAACGCAATCCCT 442
 QY 1329 ggcctcgaaacacagagcctgtgagtcacagctgagccgcatgacagatgtgagct 1388
 DB 443 GTTCGCGCTGAAACGCGCAGCAGAGTGCCTCTGTAACGCTGTAACGCGCAACCT 502
 QY 1389 gaacgacatcgcgcctagccgacatggaactggcctccaggtcctggaacgcgc 1443
 DB 503 GCACCTGCTGCTGTGAAGATGATCCTCTGTTCGCGAGGCGTGGGCTTCACC 557

Search completed: September 2, 2000, 09:52:03
 Job time: 6182 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 2, 2000, 09:56:07 ; Search time 51.59 seconds

(without alignments)
680.145 Million cell updates/sec

Title: US-09-224-556-2

Perfect score: 3005
Sequence: 1 MESSKKMDSFGALQTNPLK.....IKDDTIFIKYIVDTSLDPP 567Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 178050 seqs, 61884766 residues

Total number of hits satisfying chosen parameters: 178050

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.64:*
2: PIR1:*
3: PIR2:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2986.5	99.4	568	A55649	TNFR-associated pr
2	2980.5	99.2	568	A55960	CD40 receptor-asso
3	2859	95.1	567	I49272	CD40 receptor-asso
4	2812	93.6	543	S68467	CD40 receptor-asso
5	1182	39.3	557	JC6539	tumor necrosis fac
6	828	27.6	501	I61512	TNFR receptor asso
7	802.5	26.7	501	S56163	tumor necrosis fac
8	735.5	24.5	501	I38729	tumor necrosis fac
9	637.5	21.2	416	B55649	TNFR-associated pr
10	629	20.9	409	A54750	TNFR receptor asso
11	554	18.4	470	I38026	MN 62 protein - h
12	553.5	18.4	522	S71821	probable interleuk
13	519	17.3	509	T22238	hypothetical prote
14	189.5	6.3	458	A29361	DG17 protein - sll
15	159	5.3	852	D72230	conserved hypotet
16	151.5	5.0	634	I49642	estrogen-responsiv
17	151.5	5.0	704	A48040	meprin A (EC 3.4.2
18	150.5	5.0	1676	E71410	probable centromer
19	149	5.0	919	B72765	hypothetical prote
20	147.5	4.9	1005	A64465	hypothetical prote
21	147	4.8	609	A43906	nuclear phosphopro
22	145	4.8	1104	I38869	NFX1 - human
23	145	4.8	1300	I53799	CG1 protein - huma
24	143	4.8	1577	T19722	hypothetical prote
25	142.5	4.7	2253	T30336	nuclear/mitotic ap
26	142	4.7	1356	S32763	kinectin 1 - human
27	140	4.7	879	C71083	probable purine NT
28	140	4.7	1039	S18199	myosin heavy chain
29	139	4.6	1218	T14265	golgin-245 - mouse

30	138.5	4.6	1957	2	T38077	hypothetical colle
31	138	4.6	1690	2	T13030	microtubule bindin
32	137.5	4.6	1974	2	T30010	hypothetical prote
33	136.5	4.5	791	2	T20815	hypothetical prote
34	136.5	4.5	1187	2	T18355	hypothetical prote
35	136	4.5	698	2	S52696	myosin heavy chain
36	135.5	4.5	624	2	S28418	insulin-like growt
37	135	4.5	1607	2	T43212	probable zinc-bind
38	134.5	4.5	886	2	H69378	purine NTPase homo
39	133	4.4	944	2	S26710	spindle pole body
40	133	4.4	1249	2	H71404	hypothetical prote
41	133	4.4	1816	1	S68960	laminin alpha-4 ch
42	132.5	4.4	389	2	A40809	enamelin, 44k - bo
43	132.5	4.4	669	2	T06702	hypothetical prote
44	132	4.4	829	2	T01362	hypothetical prote
45	132	4.4	1940	1	A24922	myosin heavy chain

ALIGNMENTS

```
RESULT 1
A55649
TNFR-associated protein LAMP1 - human
N:Alternate names: CD40-binding protein
C:Species: Homo sapiens (man)
C>Date: 23-Mar-1995 #sequence-revision 23-Mar-1995 #text-change 08-Oct-1999
C:Accession: A55649; A55135
R:Mosialos, G.; Birkenbach, M.; Valamanchi, R.; Vandersdale, T.; Ware, C.; Kieff, E.
Cell 80, 389-399, 1995
A:Title: The Epstein-Barr virus transforming protein LMP1 engages signaling proteins
A:Reference number: A55649; MUID:95163092
A:Accession: A55649
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-568 <MOS>
A:Cross-references: GB:U9260; NID:6675459; PID:AAA65732.1; PID:6675460
R:Hu, H.M.; O'Rourke, K.; Boguski, M.S.; Dixit, V.M.
J. Biol. Chem. 269, 30069-30072, 1994
A:Title: A novel RING finger protein interacts with the cytoplasmic domain of CD40.
A:Reference number: A55135; MUID:95073988
A:Accession: A55135
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-133,135-404, 'G', 406-568 <HDA>
A:Cross-references: GB:U15637; NID:9595910; PID:AAA56753.1; PID:9595911
C:Superfamily: RING finger homology
C:Keywords: coiled coil; zinc
F:49-97/Domain: RING finger homology <RNG>

Query Match 99.4%; Score 2986.5; DB 2; Length 568;
Best Local Similarity 99.6%; Pred. No. 4.6e-165;
Matches 566; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MESSKKMDSFGALQTNPLKLTDRSAGTPVPEQGGYKEKFKYTVEDKXCECHVL 60
D 1 MESSKKMDSFGALQTNPLKLTDRSAGTPVPEQGGYKEKFKYTVEDKXCECHVL 60
D 1 MESSKKMDSFGALQTNPLKLTDRSAGTPVPEQGGYKEKFKYTVEDKXCECHVL 60
QY 61 CSPKTEGCHRFCSGMAALSSSPKCTACQESTVKKVFRDNCCKREILALQYICNE 120
D 61 CSPKTEGCHRFCSGMAALSSSPKCTACQESTVKKVFRDNCCKREILALQYICNE 120
D 61 CSPKTEGCHRFCSGMAALSSSPKCTACQESTVKKVFRDNCCKREILALQYICNE 120
QY 121 SRGAEQLMLGH-LVHLKNDCHFEELPCVRPDKCKEVLKDLRDHVERACKYREATCSHC 179
D 121 SRGAEQLMLGH-LVHLKNDCHFEELPCVRPDKCKEVLKDLRDHVERACKYREATCSHC 180
D 121 SRGAEQLMLGH-LVHLKNDCHFEELPCVRPDKCKEVLKDLRDHVERACKYREATCSHC 180
QY 180 KSOYPMIALQKHEDTDCVYVSCPHKCSVOTLRLSELSAHLSECVNAPSTCSFRYICV 239
D 180 KSOYPMIALQKHEDTDCVYVSCPHKCSVOTLRLSELSAHLSECVNAPSTCSFRYICV 240
D 180 KSOYPMIALQKHEDTDCVYVSCPHKCSVOTLRLSELSAHLSECVNAPSTCSFRYICV 240
QY 240 FQGNMOQIKAEHSAVQHVLLKEMSNLEKYSLLQNSVEKKSQISLHNOCSPEI 299
D 240 FQGNMOQIKAEHSAVQHVLLKEMSNLEKYSLLQNSVEKKSQISLHNOCSPEI 299
D 240 FQGNMOQIKAEHSAVQHVLLKEMSNLEKYSLLQNSVEKKSQISLHNOCSPEI 299
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Db 241 FQGTNOQIAHSSAVQVHNLKEMNSLEKKVSLQNESVEKKNKSIOSLHNOJCSFEI 300
QY 300 EIEROKEMLRNNESKILHLQVYIDSOAEKLEKDEIRPFROMWEADSMKSSVESLQNR 359
Db 301 EIEROKEMLRNNESKILHLQVYIDSOAEKLEKDEIRPFROMWEADSMKSSVESLQNR 360
QY 360 VTELESVDKSAGOVARNITGLLESQSLSRHDOMLSVHDIRLADMDLGFQVLETASYNGVLIM 419
Db 361 VTELESVDKSAGOVARNITGLLESQSLSRHDOMLSVHDIRLADMDLGFQVLETASYNGVLIM 420
QY 420 KIRDYRRRKOEAVMGKTLISYQPFYTGFGYKMCARVYLNDGDKGKTHLSLFFVIMRG 479
Db 421 KIRDYRRRKOEAVMGKTLISYQPFYTGFGYKMCARVYLNDGDKGKTHLSLFFVIMRG 480
QY 480 EYDALLPMPFKOKVITLMDQSSRRHLGDAFKPDNSSSFKKPTGEMNIASGCPVFAQ 539
Db 481 EYDALLPMPFKOKVITLMDQSSRRHLGDAFKPDNSSSFKKPTGEMNIASGCPVFAQ 540
QY 540 TVLENGTYIKDDTIFIKYIVDTSDLPDP 567
Db 541 TVLENGTYIKDDTIFIKYIVDTSDLPDP 568

```

RESULT 2

```

A55960
CD40 receptor-associated factor 1 - human
C:Species: Homo sapiens (man)
C>Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 10-Jul-1998
C:Accession: A55960
R:Cheng, G.; Cleary, A.M.; Ye, Z.S.; Hong, D.I.; Lederman, S.; Baltimore, D.
Science 267, 1494-1498, 1995
A:Title: Involvement of CRAF1, a relative of TRAF, in CD40 signaling.
A:Reference number: A55960; MUID:95184010
A:Accession: A55960
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-568 <RES>
A:Cross-references: EMBL:U21092; NID:g726087; PID:g726088
C:Genetics:
A:Gene: CRAF1
C:Superfamily: RING finger homology
C:Keywords: zinc
F:49-97/Domain: RING finger homology <RNG>

```

```

Query Match 99.2%; Score 2980.5; DB 2; Length 568;
Best Local Similarity 99.5%; Pred. No. 1e-164;
Matches 565; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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```

Db 1 MESSKMDSPGALQTNPPKLTDRSAGTPVFPVPEGGYKKEKFKVTVEDKYCKECHLYL 60
QY 61 CSPKQTECHRCESCMALLSSSPKCTACQESIVKDKVFNCKCKREILALQIYCRNE 120
Db 61 CSPKQTECHRCESCMALLSSSPKCTACQESIVKDKVFNCKCKREILALQIYCRNE 120
QY 121 SRGCAEQLMLGH-LVHLKNDCHFEELPCVAPDCKEYLRKDLRDHYEAKCKYREATCSHC 179
Db 121 SRGCAEQLMLGH-LVHLKNDCHFEELPCVAPDCKEYLRKDLRDHYEAKCKYREATCSHC 180
QY 180 KQVPMIALQKHEDTDCPCVAVSCPHKCSVQTLRLSELNAHLSSECVNAPSTCSFKRIGCV 239
Db 181 KQVPMIALQKHEDTDCPCVAVSCPHKCSVQTLRLSELNAHLSSECVNAPSTCSFKRIGCV 240
QY 240 FQGTNOQIAHSSAVQVHNLKEMNSLEKKVSLQNESVEKKNKSIOSLHNOJCSFEI 299
Db 241 FQGTNOQIAHSSAVQVHNLKEMNSLEKKVSLQNESVEKKNKSIOSLHNOJCSFEI 300
QY 300 EIEROKEMLRNNESKILHLQVYIDSOAEKLEKDEIRPFROMWEADSMKSSVESLQNR 359
Db 301 EIEROKEMLRNNESKILHLQVYIDSOAEKLEKDEIRPFROMWEADSMKSSVESLQNR 360

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```

QY 360 VTELESVDKSAGOVARNITGLLESQSLSRHDOMLSVHDIRLADMDLGFQVLETASYNGVLIM 419
Db 361 VTELESVDKSAGOVARNITGLLESQSLSRHDOMLSVHDIRLADMDLGFQVLETASYNGVLIM 420
QY 420 KIRDYRRRKOEAVMGKTLISYQPFYTGFGYKMCARVYLNDGDKGKTHLSLFFVIMRG 479
Db 421 KIRDYRRRKOEAVMGKTLISYQPFYTGFGYKMCARVYLNDGDKGKTHLSLFFVIMRG 480
QY 480 EYDALLPMPFKOKVITLMDQSSRRHLGDAFKPDNSSSFKKPTGEMNIASGCPVFAQ 539
Db 481 EYDALLPMPFKOKVITLMDQSSRRHLGDAFKPDNSSSFKKPTGEMNIASGCPVFAQ 540
QY 540 TVLENGTYIKDDTIFIKYIVDTSDLPDP 567
Db 541 TVLENGTYIKDDTIFIKYIVDTSDLPDP 568

```

RESULT 3

```

A49272
CD40 receptor-associated factor 1 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 05-Nov-1999
C:Accession: I49272
R:Cheng, G.; Cleary, A.M.; Ye, Z.S.; Hong, D.I.; Lederman, S.; Baltimore, D.
Science 267, 1494-1498, 1995
A:Title: Involvement of CRAF1, a relative of TRAF, in CD40 signaling.
A:Reference number: A55960; MUID:95184010
A:Accession: I49272
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-567 <RES>
A:Cross-references: EMBL:U21050; NID:g719292; PIDN:AACS2175.1; PID:g719293
C:Genetics:
A:Gene: CRAF1
C:Superfamily: RING finger homology
C:Keywords: zinc finger
F:48-96/Domain: RING finger homology <RNG>

```

```

Query Match 95.1%; Score 2859; DB 2; Length 567;
Best Local Similarity 95.6%; Pred. No. 1e-157;
Matches 543; Conservative 7; Mismatches 16; Indels 2; Gaps 2;

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```

QY 1 MESSKMDSPGALQTNPPKLTDRSAGTPVFPVPEGGYKKEKFKVTVEDKYCKECHLYL 60
Db 1 MESSKMDSPGALQTNPPKLTDRSAGTPVFPVPEGGYKKEKFKVTVEDKYCKECHLYL 59
QY 61 CSPKQTECHRCESCMALLSSSPKCTACQESIVKDKVFNCKCKREILALQIYCRNE 120
Db 61 CSPKQTECHRCESCMALLSSSPKCTACQESIVKDKVFNCKCKREILALQIYCRNE 119
QY 121 SRGCAEQLMLGH-LVHLKNDCHFEELPCVAPDCKEYLRKDLRDHYEAKCKYREATCSHC 179
Db 120 SRGCAEQLMLGH-LVHLKNDCHFEELPCVAPDCKEYLRKDLRDHYEAKCKYREATCSHC 179
QY 180 KQVPMIALQKHEDTDCPCVAVSCPHKCSVQTLRLSELNAHLSSECVNAPSTCSFKRIGCV 239
Db 180 KQVPMIALQKHEDTDCPCVAVSCPHKCSVQTLRLSELNAHLSSECVNAPSTCSFKRIGCV 239
QY 240 FQGTNOQIAHSSAVQVHNLKEMNSLEKKVSLQNESVEKKNKSIOSLHNOJCSFEI 299
Db 240 FQGTNOQIAHSSAVQVHNLKEMNSLEKKVSLQNESVEKKNKSIOSLHNOJCSFEI 299
QY 300 EIEROKEMLRNNESKILHLQVYIDSOAEKLEKDEIRPFROMWEADSMKSSVESLQNR 359
Db 300 EIEROKEMLRNNESKILHLQVYIDSOAEKLEKDEIRPFROMWEADSMKSSVESLQNR 359
QY 360 VTELESVDKSAGOVARNITGLLESQSLSRHDOMLSVHDIRLADMDLGFQVLETASYNGVLIM 419
Db 360 VTELESVDKSAGOVARNITGLLESQSLSRHDOMLSVHDIRLADMDLGFQVLETASYNGVLIM 419
QY 420 KIRDYRRRKOEAVMGKTLISYQPFYTGFGYKMCARVYLNDGDKGKTHLSLFFVIMRG 479
Db 420 KIRDYRRRKOEAVMGKTLISYQPFYTGFGYKMCARVYLNDGDKGKTHLSLFFVIMRG 479

```

DB 420 KIRDYKRRKQEAVMGKTLISYQPTGYGYKMCARVYLNDGKMGKTHLSLFFVIMG 479
QY 480 EYDALLPMPFKOKVITLMDQSSRRHLDAKRPDNPSSFFKPTGEMNIASGCPVFAQ 539
DB 480 EYDALLPMPFKOKVITLMDQSSRRHLDAKRPDNPSSFFKPTGEMNIASGCPVFAQ 539
QY 540 TVLENGTYIKDDTIFIKVIVDTSDLPD 567
DB 540 TVLENGTYIKDDTIFIKVIVDTSDLPD 567

RESULT 4
568467
CD40 receptor-associated protein CAP-1 - human
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998
C:Accession: S68467; I53498
R:Sato, T.; Irie, S.; Reed, J.C.
FEBS Lett. 358, 113-118, 1995
Title: A novel member of the TRAF family of putative signal transducing proteins binds
Reference number: I53498; MUID:95129692
A:Accession: S68467
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-543 <SAT>
A:Cross-references: EMBL:138509; NID:9695357; PID:9695358
A:Experimental source: tissue-type fetal brain
C:Genetics:
A:Gene: CAP-1
C:Superfamily: RING finger homology
C:Keywords: homodimer; signal transduction; zinc; zinc finger
E:49-97/Domain: RING finger homology <RNG>

Query Match 93.6%; Score 2812; DB 2; Length 543;
Best Local Similarity 94.9%; Pred. No. 4.9e-155;
Matches 539; Conservative 0; Mismatches 3; Indels 26; Gaps 2;

QY 1 MSSSKMDSGALQTNPKLHTRDSAGTPVYVEGQGYKEKVKYVEDKCKEHLV 60
DB 1 MSSSKMDSGALQTNPKLHTRDSAGTPVYVEGQGYKEKVKYVEDKCKEHLV 60
QY 61 CSPKOTEGHRCFSCSMALLSSSPKCTACOBSTYKDYVFNDCKRETLAQIYCRNE 120
DB 61 CSPKOTEGHRCFSCSMALLSSSPKCTACOBSTYKDYVFNDCKRETLAQIYCRNE 120
QY 121 SSGCAEQMLGHLVHLKNDCHFEELPCVPRDCKEYLRKDLRDHYEKACKYREATCSHC 179
DB 121 SSGCAEQMLGHLVHLKNDCHFEELPCVPRDCKEYLRKDLRDHYEKACKYREATCSHC 180
QY 180 KQGVPMIALQKHEDDPCVVVSCPHKCSVQITLRSLSNAHSECVNADSTGCFKRYGCV 239
DB 181 KQGVPMIALQKHEDDPCVVVSCPHKCSVQITLRSLSNAHSECVNADSTGCFKRYGCV 239
QY 240 FGTNNOITAHESAVOHVNLKEMNSLEKVSLLQNESVEKNKSIOSLHNOISFET 299
DB 240 FGTNNOITAHESAVOHVNLKEMNSLEKVSLLQNESVEKNKSIOSLHNOISFET 299
QY 218 --GTNNOITAHESAVOHVNLKEMNSLEKVSLLQNESVEKNKSIOSLHNOISFET 275
DB 218 --GTNNOITAHESAVOHVNLKEMNSLEKVSLLQNESVEKNKSIOSLHNOISFET 275
QY 300 ETEROKEMLRNNSKILHQRVIDSOAEKLEKELRPFROMWEADSKSSVESLQNR 359
DB 276 ETEROKEMLRNNSKILHQRVIDSOAEKLEKELRPFROMWEADSKSSVESLQNR 355
QY 360 VTELESVDKSAGOVANNTGLLESQLSRHDQMLSVHDIRLADMDLGFQVLETASVGLTW 419
DB 336 VTELESVDKSAGOVANNTGLLESQLSRHDQMLSVHDIRLADMDLGFQVLETASVGLTW 395
QY 420 KIRDYKRRKQEAVMGKTLISYQPTGYGYKMCARVYLNDGKMGKTHLSLFFVIMG 479
DB 396 KIRDYKRRKQEAVMGKTLISYQPTGYGYKMCARVYLNDGKMGKTHLSLFFVIMG 455
QY 480 EYDALLPMPFKOKVITLMDQSSRRHLDAKRPDNPSSFFKPTGEMNIASGCPVFAQ 539
DB 456 EYDALLPMPFKOKVITLMDQSSRRHLDAKRPDNPSSFFKPTGEMNIASGCPVFAQ 515

QY 540 TVLENGTYIKDDTIFIKVIVDTSDLPD 567
DB 516 TVLENGTYIKDDTIFIKVIVDTSDLPD 543

RESULT 5
J66539
tumor necrosis factor receptor-associated factor 5 homolog - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 17-Mar-1999
R:Mizushima, S.; Fujita, M.; Ishida, T.; Azuma, S.; Kato, K.; Hirai, M.; Otsuke, M.;
Gene 207, 135-140, 1998
A:Title: Cloning and characterization of a cDNA encoding the human homolog of tumor n
A:Reference number: J66539; MUID:98172745
A:Accession: J66539
A:Molecule type: mRNA
A:Residues: 1-557 <MT>
A:Cross-references: DDBJ:AB000509
C:Comment: This protein is involved in transduction of signals from various tumor nec
phoroxin-beta receptor.
C:Genetics:
A:Map position: 1q32.3-1q41.1
C:Keywords: coiled coil; tumor; zinc finger

Query Match 39.3%; Score 1182; DB 2; Length 557;
Best Local Similarity 41.6%; Pred. No. 4.4e-61;
Matches 229; Conservative 121; Mismatches 181; Indels 20; Gaps 8;

QY 25 RSAGTPVYVEGQGYKEKVKYVEDKCKEHLVYCSKQTECGHRCFSCSMALLS-S 83
DB 17 QNSGNSISLDFPESLEYOVERLEERYKCAFCHSVLHNPQCGHRCFOCHTSLRELN 76
QY 84 SPSKACQESTYKDKVFNDCKRETLAQIYCRNESGCAEQMLGHLVHLKNDCHFE 143
DB 77 TYPICPVNKEVILKQDEVFNDCCKREVLYLVCN-AGCAKAVILGKQDHLQOCLQ 135
QY 144 ELPVPRDCKEYLRKDLRDHYEKACKYREATCSHCKSGVPMIALQKHEDDPCVVVSC 203
DB 136 PVQSNKRECPVLRKDLREHLASQCFKREKLYCKQVVVYINQNHENLCEPVPVC 195
QY 204 PHKCSVQITLRSLSNAHSECVNADSTGCFKRYGCVFQSTNQOIKAHESAVOHVNLK 263
DB 196 PNNCA-KIILKTEVDENHLAVCEAEODCPFKHYGCAVTDKRRRLQOHSALREHRLV 254
QY 264 EMSNLEKVSLLQNESVEKNKSIOSLHNOISFETIEIEROKEMLRNNSKILHQRVID 323
DB 255 EKNVQLEQISDLHKSLEQESKIQDLAETIKLEKEFKQFQOLFGKNSFLPNID-VFA 313
QY 324 SOAEKLEKELRPF-----RQNWEEADSKSSVESLQNRTELESVDKSAGVARNY 377
DB 314 SHIDKSAWLEAQVHQLQVNOQNKFDRLPLMEANDVYKOKITLLEND-----QRL 366
QY 378 GLLESQLSRHDQMLSVHDIRLADMDLGFQVLETASVGLTWIKIRDYKRRKQEAVMGKTL 437
DB 367 AVLEETNKHHDHINIKHQAOLSKNEREFKLEGTCTYNGKILWVVDYKKKKRAVAGHTV 426
QY 438 SLYSQPTGYGYKMCARVYLNDGKMGKTHLSLFFVIMRGYDALLPMPFKOKVITLMD 497
DB 427 SLFSQPTGYSGGYRLCAAYLNGDSSGSHSLTFVNRGEFDSLLQMPFRQVYTLWL 486
QY 498 MDQSSRRHLDAKRPDNPSSFFKPTGEMNIASGCPVFAQVLEEN--GTAYIKDDTIF 555
DB 487 LQV-SGKKNIMETFKRPDNPSSFFKRDGEMNIASGCPRVAVSLVLEMANAYIKDDTIFL 545
QY 556 KYIVDTSDLPD 566
DB 546 KVAVDTDLDD 556

RESULT 6

161512
TNF receptor associated factor 2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: 161512
R:Rothe, M.; Wong, S.C.; Henzel, W.J.; Goeddel, D.V.
Cell 78, 681-692, 1994
A:Title: A novel family of putative signal transducers associated with the cytoplasmic d
A:Reference number: A54750; MUID:94349371
A:Accession: 161512
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-501 <RES>
A:Cross-references: GB:I35303; NID:9532620; PIDN:AAC37662.1; PID:9532621
C:Genetics:
A:Gene: TRAF2
C:Superfamily: RING finger homology
C:Keywords: zinc
F:30-78/Domain: RING finger homology <RNG>

Query Match 27.6%; Score 828; DB 2; Length 501;
Best Local Similarity 33.4%; Pred. No. 9, 9e-41;
Matches 196; Conservative 90; Mismatches 190; Indels 110; Gaps 19;

QY 3 SSKKMDSPGALQTNPIKHTDSAGTPVFPDGGYKEKFKVT-VEDKYKCEKHLVLC 61
DB 2 AASVTSFGSLELDP-----GFSKTLGTREAKYLCSACKNRLR 42
QY 62 SPQTEGCHRFCESSCMALLSSSPKCTAC-----QESI---VKDFVFNCKCKREILA 112
DB 43 RPPDQAGCHRCFCLSISSGPNCAACYBEYBEGISILESSAFDNARRVES 102
QY 113 LQIYCRNESGCAEQMLGHLVHLKNDCHFEELPCVR---PDCEKYLKDLNDHYEKAC 169
DB 103 LPAPCPMD--GCTWK---GTLKEYES-CHGELCPFLTECPACKGLRLSEKEHTEBOEC 156
QY 170 KYRPAATSHCKSQVPYMLALQKHEITDPCVYVSGPHKCSQVTLRLSLSHLSFCVNAVS 229
DB 157 PKRSLSCOHCRAPCSHVDLEHYHEV-CPKRPPLTC-DGCGKKKIPRETFDDHVRACSKCRY 214
QY 230 TCSKRRGCVQGTNOQIKAHSSAVOHVNLKEMNSLEKVS-----LLQNE 279
DB 215 LCRHYVGCSEMTENLOHDELRLRLEHALL--LSFLEAQSPTLQVYPELLQRC 272
QY 280 SVEKNKSIQSLHQISFEIEIEROKEMLRNNEKIIHLQRYDSQAEKLEKIDKEIRPF 339
DB 273 QILROK-IAPFENIVCVLNFREVER-----VAVTAEACSRQHRLDOD--- 312
QY 340 RQNNEDADSKSSVESLQNRVTELESYDKSAGQVARNGTGLLESQLSHRDQLSVHDRLA 399
DB 313 -----KTEALSNKVOOLE-----RSIGL-----KDLAMA 336
QY 400 DMDLGQVLEIETASYNGVLIWKIRDYKRRKQEAANGKTLSTYSOFTYGYGFKMCARYTL 459
DB 337 DLDEQVSELESTYDGVYIKWISDFTRKQEAAGRPALISPAFYSRYCYKCKLRYLL 396
QY 460 NGDNGKGTHTLSFFVYMRGEYDALLPFPFOQKVTLMMDOGSSRRHLDGAFKDPNSSL 519
DB 397 NGDSTGRGTHLSLFFVYMKKGPNDAILOPFPQKVTLMMLDHN-NRREHVIDAFRDVYSS 455
QY 520 FKRPTEGNINAGCVFAQVYLE-NGTYIKDDTIFIKVIYDTSDL 564
DB 456 FQRPVSDMNINAGCPDFCPVSKMEAKNSYVADDAIFAIYDITGL 501

RESULT 7
S56163
tumor necrosis factor receptor-associated protein - human
N:Alternate names: TNF receptor-associated protein
C:Species: Homo sapiens (man)
C:Date: 10-Oct-1995 #sequence_revision 01-Dec-1995 #text_change 08-Oct-1999
C:Accession: S56163; S58925; S58926

R:Song, H.Y.; Donner, D.B.
Biochem. J. 309, 825-829, 1995
A:Title: Association of a RING finger protein with the cytoplasmic domain of the huma
A:Reference number: S56163; MUID:95366958
A:Accession: S56163
A:Molecule type: mRNA
A:Residues: 1-501 <SON>
A:Cross-references: EMBL:U12597
R:Song, H.Y.; Donner, D.
submitted to the EMBL Data Library, July 1994
A:Description: Association of a RING finger protein with the cytoplasmic domain of th
A:Reference number: S58925
A:Accession: S58925
A:Molecule type: mRNA
A:Residues: 1-42, 63-342, 363-501 <SOW>
A:Cross-references: EMBL:U12597
A:Accession: S58926
A:Molecule type: mRNA
A:Residues: 1-342, RPPDQAGCHRCFCLASIL', 363-501 <SOF>
A:Cross-references: EMBL:U12597; NID:975272; PIDN:AAAB7706.1; PID:975273
C:Superfamily: RING finger homology
C:Keywords: zinc finger
F:30-78/Domain: RING finger homology <RNG>

Query Match 26.7%; Score 802.5; DB 2; Length 501;
Best Local Similarity 35.3%; Pred. No. 2, 9e-39;
Matches 196; Conservative 87; Mismatches 176; Indels 97; Gaps 22;

QY 36 QGGYKEKFKVT-VEDKYKCEKHLVLCSPKQTEGCHRFCESSCMALLSSSPKCTAC-OE 93
DB 16 QGFSKTLGTREAKYLCSACKNRLRPPDQAGCHRCFCLSISSGPNCAACYHE 75
QY 94 STYKDY-----FKDCCCKREILAQIYCRNRSRCAEQMLGHLVHLKNDCHFEEL 145
DB 76 GYIEEGISILESSAFPDNARRVESLPAVC--PSDGTWK---GTLKEYES-CHGRC 129
QY 146 PCVR---PDCEKYLKDLNDHYEKACRYEATCSCKSQVPYMLALQKHEITDPCVYVS 202
DB 130 PLMLTGPCRACKGLVRLGEKEHRLHEHCPRSLSCRRCAPCGADVKAHVEY-CPKPLT 188
QY 203 CPKCSQVQTLNSELSEAHLSFCVNAVSTCSFKRYGV--FQGTNOQIRAHSSAVOHVN 260
DB 189 C-DGCGKKKIPREKFDHVKTCGRVPCRFHAIQLETVBEKQD--EHEVQMLREHLA 245
QY 261 LKEMNSLEK-----VSLQN-ESEYKKNKSIQSLNQICSEFEIEEROKEMLR 309
DB 246 ML--LSSVLEAKFLGDQSHAGSELLQRCSELEKTA--TFENIVCVLNFREVER----- 295
QY 310 NNEKIIHLQRYDSQAEKLEKIDKEIRPFRQNNEDADSKSSVESLQNRVTELESYDKS 369
DB 296 -----VAVTAEACS-----RQHRLDOD---KTEALSNKVOOLE----- 325
QY 370 AGQVARNGTGLLESQLSRHDMQSVHDIRLADMDLGQVLEIETASYNGVLIWKIRDYKRRKQ 429
DB 326 -----RSIGL-----KDLAMADLEQKYLEEASTYDVFVLTISDFPRKQLQ 366
QY 430 EAVMGKTLISQPFYTGFGYKMCARYTLNGDMGKGTHTLSLFFVYMRGEYDALLPMPF 489
DB 367 EAVAGRPALISPAFYSRYCYKCKLRYLLNDGQIRGHTLSLFFVYMRGPNDAILRWPF 426
QY 490 KQRYTLMDOGSSRRHLDGAFKDPNSSLFFKPTGEANINAGCPVFAQVYLE-NGTYI 548
DB 427 NQKVTLMMLDQ-NRREHVIDAFRDVYSSSFQRPVSDMNINAGCPDFCPVSKMEAKNSYV 485
QY 549 KDDTIFIKVIYDTSDL 564
DB 486 RDDAIFKATVYDITGL 501

RESULT 8
I38729
tumor necrosis factor type 2 receptor associated protein 3 - human

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 2, 2000, 10:21:48 ; Search time 38.17 Seconds

(without alignments)
460.331 Million cell updates/sec

Title: US-09-224-556-2

Perfect score: 3005

Sequence: 1 MESSKRMDSFGALQTNPLK.....IKDDTIFIKYIVDTSLDPP 567

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 85661 seqs, 30989116 residues

Total number of hits satisfying chosen parameters: 85661

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2960.5	99.2	568	1	TRA3_HUMAN
2	2859	95.1	567	1	TRA3_MOUSE
3	828	27.6	501	1	TRA2_MOUSE
4	735.5	24.5	501	1	TRA2_HUMAN
5	637.5	21.2	416	1	TRA1_HUMAN
6	629	20.9	409	1	TRA1_MOUSE
7	189.5	6.3	458	1	DG17_DICDI
8	151.5	5.0	704	1	MEPB_MOUSE
9	145	4.8	1104	1	NFX1_HUMAN
10	140.5	4.7	624	1	A33_PLENA
11	140	4.7	1102	1	MSC_CHICK
12	140	4.7	3210	1	CENF_HUMAN
13	138.5	4.6	1957	1	YD86_SCHPO
14	136	4.5	704	1	MEPB_RAT
15	135	4.5	1607	1	MIPR_LYMET
16	133	4.4	944	1	NKPL_YEAST
17	132.5	4.4	389	1	ENAM_BOVIN
18	132	4.4	1940	1	MSE_RAT
19	131.5	4.4	724	1	HMR_HUMAN
20	131.5	4.4	1679	1	Y109_YEAST
21	131	4.4	1940	1	MYSE_HUMAN
22	130.5	4.3	1928	1	MYSL_YEAST
23	130	4.3	1106	1	STC_DROME
24	130	4.3	1940	1	MYSE_CHICK
25	129.5	4.3	1225	1	SMC1_YEAST
26	129	4.3	700	1	MEPB_HUMAN
27	129	4.3	1816	1	LM44_HUMAN
28	128.5	4.3	285	1	TPM1_DROME
29	128.5	4.3	504	1	TPM5_DROME
30	128.5	4.3	518	1	TPM4_DROME
31	127	4.2	1290	1	KCP4_XENLA
32	127	4.2	1939	1	MYSA_HUMAN
33	126.5	4.2	283	1	TPMM_LOCOMI

34	126	4.2	252	1	TPM3_DROME
35	126	4.2	747	1	MEPB_MOUSE
36	125	4.2	794	1	HMR_MOUSE
37	125	4.2	1073	1	RAG1_ONCMX
38	125	4.2	1084	1	MYSS_RABIT
39	125	4.2	1863	1	BRCL_HUMAN
40	125	4.2	2663	1	CENF_HUMAN
41	124.5	4.1	1935	1	MYSB_RAT
42	124	4.1	748	1	MEPB_RAT
43	124	4.1	1039	1	YAF3_SCHPO
44	123.5	4.1	783	1	ZFY2_MOUSE
45	123.5	4.1	876	1	MYSS_HUMAN

ALIGNMENTS

RESULT ID	TRA3_HUMAN	STANDARD	PRT	568 AA.
AC	Q1314: Q13076; Q13947; Q12990;			
DT	15-FEB-2000 (Rel. 38, Created)			
DT	15-FEB-2000 (Rel. 39, Last sequence update)			
DT	15-FEB-2000 (Rel. 39, Last annotation update)			
DE	TNF RECEPTOR ASSOCIATED FACTOR 3 (CD40 RECEPTOR ASSOCIATED FACTOR 1)			
DE	(CRAFT) (CD40 BINDING PROTEIN) (CD40BP) (LMP1 ASSOCIATED PROTEIN)			
DE	(LAP1)			
GN	TRA3 OR CRAFT OR CAP-1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
RN	[1]			
RP	SEQUENCE FROM N. A.			
RA	Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.,			
RT	"Involvement of CRAFT, a relative of TRAF, in CD40 signaling."			
RL	Science 267:1494-1498(1995).			
RN	[2]			
RP	SEQUENCE FROM N. A., AND CHARACTERIZATION.			
RC	TISSUE-LYMPHOMA;			
RX	MEDLINE: 95163092.			
RA	Mosialos G., Birkbach M., Yamanchilli R., Vandersdale T., Ware C.,			
RT	Kieff E.;			
RL	"The Epstein-Barr virus transforming protein LMP1 engages signaling proteins for the tumor necrosis factor receptor family."			
RN	[3]			
RP	SEQUENCE FROM N. A.			
RC	TISSUE-FETAL BRAIN;			
RX	MEDLINE: 95129692.			
RA	Sato T., Irie S., Reed J.C.;			
RT	"A novel member of the TRAF family of putative signal transducing proteins binds to the cytosolic domain of CD40."			
RL	FEBS Lett. 358:113-118(1995).			
RN	[4]			
RP	SEQUENCE FROM N. A.			
RX	MEDLINE: 95073988.			
RA	Hu H.M., O'Rourke K., Boguski M.S., Dixit V.M.;			
RT	"A novel RING finger protein interacts with the cytoplasmic domain of CD40."			
RL	J. Biol. Chem. 269:30669-30672(1994).			
CC	- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN OF THE 75 KDA TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2). ALSO BINDS TO CD40 AND THE LYMPHOTOXIN-BETA RECEPTOR.			
CC	- SUBUNIT: HOMODIMER OR HETERODIMER WITH OTHER TNF RECEPTOR ASSOCIATED FACTORS (POTENTIAL).			
CC	- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.			
CC	- SIMILARITY: CONTAINS A MATH/TRAFF DOMAIN.			
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CC EMBL; U21092; AAC5012.1; -
 DR EMBL; U19260; AAA65732.1; -
 DR EMBL; L38509; AAA68195.1; -
 DR EMBL; U15637; AAA56753.1; -
 DR MIM; 601896; -
 DR PFM; PF00917; MATH; 1.
 DR PFM; PF00917; ZF-C3HC4; 1.
 DR PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
 KW Zinc-finger; Coiled coil.
 FT ZN FING 68 77 C3HC4-TYPE.
 FT DOMAIN 267 338 COILED COIL (POTENTIAL).
 FT CONFLICT 129 129 MATH/TRAF.
 FT CONFLICT 134 134 T->M (IN REF. 2 AND 4).
 FT CONFLICT 218 242 MISSING (IN REF. 4).
 FT CONFLICT 339 339 MISSING (IN REF. 3).
 FT CONFLICT 405 405 P->S (IN REF. 3).
 FT CONFLICT 405 405 R->G (IN REF. 4).
 SEQUENCE 568 AA; 64460 MW; 6765333FBF53308B CRC64;

Query Match 99.2%; Score 2980.5; DB 1; Length 568;
 Best Local Similarity 99.5%; Pred. No. 1.2e-172;
 Matches 565; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MESSKMDSPGALQTPNPKLHTDRSAGTPVPEVPGGKKEKFKVTVEDKCYKCECHLV 60
 DB 1 MESSKMDSPGALQTPNPKLHTDRSAGTPVPEVPGGKKEKFKVTVEDKCYKCECHLV 60
 QY 61 CSPKOTEGCHRCESCMALLSSSPKCTACQESTYKDVVFVFNCKRREILALQYCRNE 120
 DB 61 CSPKOTEGCHRCESCMALLSSSPKCTACQESTYKDVVFVFNCKRREILALQYCRNE 120
 QY 121 SSGCAEQLMIGH-LVHLKNDCHFEELPCVRPDCKEYVLRKDLADHYEKACKYREATCSNC 179
 DB 121 SSGCAEQLMIGH-LVHLKNDCHFEELPCVRPDCKEYVLRKDLADHYEKACKYREATCSNC 180
 QY 121 SSGCAEQLMIGH-LVHLKNDCHFEELPCVRPDCKEYVLRKDLADHYEKACKYREATCSNC 180
 DB 121 SSGCAEQLMIGH-LVHLKNDCHFEELPCVRPDCKEYVLRKDLADHYEKACKYREATCSNC 180
 QY 180 KSOVPMIALQKHEDIDPCVNVVSCPHKCSVQTLNSELSELSAHLSECVNADSTCSFKRYGCV 239
 DB 180 KSOVPMIALQKHEDIDPCVNVVSCPHKCSVQTLNSELSELSAHLSECVNADSTCSFKRYGCV 240
 QY 181 KSOVPMIALQKHEDIDPCVNVVSCPHKCSVQTLNSELSELSAHLSECVNADSTCSFKRYGCV 240
 DB 181 KSOVPMIALQKHEDIDPCVNVVSCPHKCSVQTLNSELSELSAHLSECVNADSTCSFKRYGCV 240
 QY 240 FCGTNOQIATRAHSSAVQVNVNLLKEMNSLEKKVSLLOHSEVEKNKSISLOLNQICSEFI 299
 DB 240 FCGTNOQIATRAHSSAVQVNVNLLKEMNSLEKKVSLLOHSEVEKNKSISLOLNQICSEFI 300
 QY 241 FCGTNOQIATRAHSSAVQVNVNLLKEMNSLEKKVSLLOHSEVEKNKSISLOLNQICSEFI 300
 DB 241 FCGTNOQIATRAHSSAVQVNVNLLKEMNSLEKKVSLLOHSEVEKNKSISLOLNQICSEFI 300
 QY 300 EIEROKEMLRNNEKSLIHLQVYIDSOAEKLEKELRPFPRONWEADSMKSSVESLQNR 359
 DB 301 EIEROKEMLRNNEKSLIHLQVYIDSOAEKLEKELRPFPRONWEADSMKSSVESLQNR 360
 QY 360 VTELESVDKSAGVARNGLILSLSQSLSRHDOMLSVHDIRLADMDLGRFVLETSYNGVLIM 419
 DB 361 VTELESVDKSAGVARNGLILSLSQSLSRHDOMLSVHDIRLADMDLGRFVLETSYNGVLIM 420
 QY 420 KIRDRYKRRQAEVAMGKTLISLYSOPFTYGFYGYKMCARVYLNDGSKGKHLISFTYIMNG 479
 DB 421 KIRDRYKRRQAEVAMGKTLISLYSOPFTYGFYGYKMCARVYLNDGSKGKHLISFTYIMNG 480
 QY 480 EYDALLPFPFKOKVTLMLNDGSSRRHLGDAFPDPNSSSFKPTGEMNITAGSCPFFVAO 539
 DB 481 EYDALLPFPFKOKVTLMLNDGSSRRHLGDAFPDPNSSSFKPTGEMNITAGSCPFFVAO 540
 QY 540 TVLENGTYIKDDTIFIKVIVTSDLPD 567
 DB 541 TVLENGTYIKDDTIFIKVIVTSDLPD 568

RESULT 2
 TRA-MOUSE 567 AA.
 ID TRA-MOUSE
 AC Q0803; Q62380; STANDARD; PRT; 567 AA.

DT 15-FEB-2000 (Rel. 39, Created)
 DT 15-FEB-2000 (Rel. 39, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE TNF RECEPTOR ASSOCIATED FACTOR 3 (CD40 RECEPTOR ASSOCIATED FACTOR 1)
 DE (CRAFT) (TRAFAMN).
 DE TRAF3 OR CRAFT OR TRAFAMN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 95184010.
 RX Cheng G., Cleary A.M., Ye Z., Hong D.I., Lederman S., Baltimore D.;
 RT "Involvement of CRAFT, a relative of TRAF, in CD40 signaling.";
 RL Science 267:1494-1498(1995).
 RN [2]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RC STRAIN-C57BL/6J; TISSUE-BRAIN;
 RX MEDLINE; 96299439.
 RA Wang X., Bornslaeger E.A., Haub O., Tomihara-Newberger C., Lonberg N.,
 RA Dinulos M.B., Distche C.M., Copeland N., Gilbert D.J., Jenkins N.A.,
 RA Lacy E.;
 RT "A candidate gene for the amnionless gastrulation stage mouse mutation
 RT encodes a TRAF-related protein.";
 RL Dev. Biol. 177:274-290(1996).
 CC - FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN
 CC OF THE 75 KDA TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2). ALSO BINDS
 CC TO CD40 AND THE LYMPHOXIN-BETA RECEPTOR (BY SIMILARITY).
 CC - SUBUNIT: HOMODIMER OR HETERODIMER WITH OTHER TNF RECEPTOR
 CC ASSOCIATED FACTORS (POTENTIAL).
 CC - TISSUE SPECIFICITY: IN ADULT, HIGHEST IN BRAIN. ALSO FOUND IN
 CC KIDNEY, HEART, THYMUS, SPLEEN, LUNG, MUSCLE, TESTIS AND OVARY. NOT
 CC FOUND IN LIVER.
 CC - DEVELOPMENTAL STAGE: IN THE EMBRYO, EXPRESSED FROM 6.5. HIGHEST
 CC LEVELS FOUND BETWEEN E11.5 AND E13.5. AT LATE STAGES OF GESTATION,
 CC FROM E14.5, ONLY LOW LEVELS ARE DETECTED.
 CC - SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
 CC - SIMILARITY: CONTAINS A MATH/TRAF DOMAIN.
 CC
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Query Match 95.1%; Score 2859; DB 1; Length 567;
 Best Local Similarity 95.6%; Pred. No. 2.5e-155;
 Matches 543; Conservative 7; Mismatches 16; Indels 2; Gaps 2;
 QY 1 MESSKMDSPGALQTPNPKLHTDRSAGTPVPEVPGGKKEKFKVTVEDKCYKCECHLV 60
 DB 1 MESSKMDSPGALQTPNPKLHTDRSAGTPVPEVPGGKKEKFKVTVEDKCYKCECHLV 59
 QY 61 CSPKOTEGCHRCESCMALLSSSPKCTACQESTYKDVVFVFNCKRREILALQYCRNE 120
 DB 60 CSPKOTEGCHRCESCMALLSSSPKCTACQESTYKDVVFVFNCKRREILALQYCRNE 119

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OY 121 SRGAEOLMLGH-LVHLKNDCHFEELPCVYRDPCKEYLRKDLRDHYERAKCYREARCSHC 179
DB 120 GRCGEOLTLGLVHLKNECOFEEELPCURADCKEYLRKDLRDHYERAKCYREARCSHC 179
OY 180 KSOVMIALQKHEDTDCPCVVSCHPKSCVQTLRLSELSEHLSECVNAPSTCSFRKRGCV 239
DB 180 KSOVMIALQKHEDTDCPCVVSCHPKSCVQTLRLSELSEHLSECVNAPSTCSFRKRGCV 239
OY 240 FQGTNOQIKAHBASSAVQHNLKEMSNSELEKRVSLQNESEYKKNISQSLNNOICSEFI 299
DB 240 FQGTNOQIKAHBASSAVQHNLKEMSNSELEKRVSLQNESEYKKNISQSLNNOICSEFI 299
OY 300 EIEREKEMRNNESTKLHLQRYIDSAEKLDELKEIRFRONWEADSKSSVESLQNR 359
DB 300 EIEREKEMRNNESTKLHLQRYIDSAEKLDELKEIRFRONWEADSKSSVESLQNR 359
OY 360 VTELESVDKASGOVANTGLLESOLSRHDOMLSVHDIRLADMDLGFQVLETSYNGVLIM 419
DB 360 VTELESVDKASGOVANTGLLESOLSRHDOMLSVHDIRLADMDLGFQVLETSYNGVLIM 419
OY 420 KIRDYKRRKQEAVMGKTLISYQPFYTGFGYKMCARYLNGDMGKGTLSLFEVIMRG 479
DB 420 KIRDYKRRKQEAVMGKTLISYQPFYTGFGYKMCARYLNGDMGKGTLSLFEVIMRG 479
OY 480 EYDALLPWFKRVKVTLMMDQSSRRHLGDAFRPNSSSFKKPGEMNIIASGCPYFAVQ 539
DB 480 EYDALLPWFKRVKVTLMMDQSSRRHLGDAFRPNSSSFKKPGEMNIIASGCPYFAVQ 539
OY 540 TVLENGTYIKDITFIKVIYVTSDDLPP 567
DB 540 TVLENGTYIKDITFIKVIYVTSDDLPP 567

```

RESULT 3

```

ID TRAF2_MOUSE STANDARD: PRT: 501 AA.
AC P39429:
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE TNF RECEPTOR ASSOCIATED FACTOR 2 (TRAF2).
GN TRAF2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
SEQUENCE FROM N.A.
MEDLINE: 94349371.
RA Rothe M., Wong S.C., Henzel W.J., Goeddel D.V.:
RT "A novel family of putative signal transducers associated with the
RT cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";
RL Cell 78:681-692(1994).
CC -1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN
CC OF THE 75 KDA TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2) AND
CC ACTIVATES NF-KAPPA-B.
CC -1- SUBUNIT: HOMODIMER OR HETERODIMER OF TRAF1 AND TRAF2. THIS
CC HETERODIMER CAN BIND TO THE N-TERMINAL OF INHIBITOR OF APOPTOSIS
CC PROTEINS 1 AND 2 (IAPs), TO RECRUIT THEM TO THE TUMOR NECROSIS
CC FACTOR RECEPTOR 2 (TNFR2).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
CC -1- SIMILARITY: CONTAINS A MATH/TRAF DOMAIN.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC EMBL, L35303; AAC37662.1;

```

```

DR MGD: MGI:101835; TRAF2.
DR PFAM: PF000917; MATH: 1.
DR PFAM: PF000917; ZF-C3HC4, 1.
DR PROSITE: PS00518; ZINC_FINGER_C3HC4, 1.
FW Zinc-finger; Coiled coil.
FW 2N_FING 34 72 C3HC4-TYPE.
FW DOMAIN 298 348 COILED COIL (POTENTIAL).
FW DOMAIN 334 501 MATH/TRAF.
SQ SEQUENCE 501 AA: 56026 MW: 043B391180365F10 CAC64;

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Query Match 27.6%; Score 828; DB 1; Length 501;
 Best Local Similarity 33.4%; Pred. No. 4.2e-43;
 Matches 196; Conservative 90; Mismatches 190; Indels 110; Gaps 19;

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OY 3 SSKKMDSPGALQTNPLKLTHTDSAGTPVPEQGYKEKFEVKT-VEDKYKCKEHLVLC 61
DB 2 AASVTSFGSLTLQP-----GFSITLGLRLKAYLCSACKNLR 42
OY 62 SPKQTECGHRCFESCMALLSSSPKCTAC-----QESI---VADKYKNDCKREILA 112
DB 43 RPFQACGHRYSFCLTSLSSGPONCAQVYEGLYEEGISILESSSAPPDNAAREVYS 102
OY 113 IQIYCRNBSRGCAEOLMLGHLVHLKNDCHFEELPCVR--PPCKEYLRKDLRDHYERAK 169
DB 103 LPAVCPND--GCTWK---GTLKEYES-CHGGLCPFLITCPACKGLVRLSEKHEHTDEC 156
OY 170 KYREATSCHKQVPMIALQKHEDTDCPCVVSCHPKSCVQTLRLSELSEHLSECVNAPS 229
DB 157 PKRSLSCGHRAPCSHVDEHYEV-CPKFPILC-DGCGKKIIPRETFQDHYRACSKCV 214
OY 230 TCSFKRYGCVPGTNOQIKAHBASSAVQHNLKEMSNSELEKRV-----LQNE 279
DB 215 LCRFHTVGCSEWETEMQDHELQRLREHLALL--LSFLQASGTLNOVGPPELLQRC 272
OY 280 SYEKNSIQSLNNOICSEFIEIEROKEMLRNNESTKLHLQRYIDSAEKLDELKEIRFP 339
DB 273 QLEBOK-TAFENIYCVLREVER-----VAATACSKQHRLLDP--- 312
OY 340 RONWEADSKSSVESLQNRVTELESVDKASGOVANTGLLESOLSRHDOMLSVHDIRLA 399
DB 313 -----KIEALSKVQGLE-----RSISL-----KOLANA 336
OY 400 DMDLGFQVLETSYNGVLIMKIRDYKRRKQEAVMGKTLISYQPFYTGFGYKMCARYL 459
DB 337 DIEQKVSLEVTYDGVFVWKISDFTKROEAVAGTRPAIFSPAFYTSRYGKMCARYL 396
OY 460 NGDMGKGTLSLFEVIMRGEDALLPMPFKQKVTLMMDQSSRRHLGDAFRPNSS 519
DB 397 NKGDSGRGHTLSLFEVIMRGEDALLPMPFKQKVTLMMDQSSRRHLGDAFRPNSS 455
OY 520 FKRPTEGEMNIIASGCPYFAVQVLE-NGTYIKDITFIKVIYVTSDDL 564
DB 456 FORPVDNIIASGCPYFAVQVLE-NGTYIKDITFIKVIYVTSDDL 501

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RESULT 4

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ID TRAF2_HUMAN STANDARD: PRT: 501 AA.
AC Q12933:
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE TNF RECEPTOR ASSOCIATED FACTOR 2 (TRAF2) (TUMOR NECROSIS FACTOR TYPE 2
DE RECEPTOR ASSOCIATED PROTEIN 3).
GN TRAF2 OR TRAF3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
[1]
SEQUENCE FROM N.A.
RX MEDLINE: 95366958.
RA Song H.Y., Donner D.B.:

```

RT "Association of a RING finger protein with the cytoplasmic domain of
 RT the human type-2 tumour necrosis factor receptor."
 RT Biochem. J. 309:825-829(1995).
 [2]
 RP SEQUENCE OF 201-501 FROM N.A.
 RX MEDLINE: 94349371.
 RX Rothe M., Wong S.C., Henzel W.J., Goeddel D.V.:
 RT "A novel family of putative signal transducers associated with the
 RT cytoplasmic domain of the 75 kDa tumor necrosis factor receptor."
 RT Cell 78:681-692(1994).
 CC -1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN
 CC OF THE 75 KDA TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2) AND
 CC ACTIVATES NF-KAPPA-B.
 CC -1- SUBUNIT: HOMODIMER OR HETERODIMER OF TRAF1 AND TRAF2. THIS
 CC HETEROCOMPLEX CAN BIND TO THE N-TERMINAL OF INHIBITOR OF APOPTOSIS
 CC PROTEINS 1 AND 2 (IAPs), TO RECRUIT THEM TO THE TUMOR NECROSIS
 CC FACTOR RECEPTOR 2 (TNFR2).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
 CC -1- SIMILARITY: CONTAINS A MATH/TRAF DOMAIN.
 CC
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 CC
 CC EMBL: U12597; AAA87706.1; -
 CC DR PFM: PF00917; MATH; 1.
 CC DR PFM: PF00917; zf-C3HC4; 1.
 CC DR PROSITE: PS00518; ZINC_FINGER_C3HC4; 2.
 CC DR ZINC_FINGER; Coiled coil.
 CC ZN_FING 34 72 C3HC4-TYPE.
 CC FT DOMAIN 289 348 COILED COIL (POTENTIAL).
 CC FT DOMAIN 334 301 MATH/TRAF.
 CC FT CONFLICT 343 365 RPFQACCHRCVSCFCLASITLRLK ->
 CC FT LEMASTIDGPIFKIKISPFARK (IN REF. X).
 CC
 CC SEQUENCE 501 AA; 55794 MW; 8883651EBE20743 CRC64;
 SQ

Query Match 24.5%; Score 735.5; DB 1; Length 501;
 Best Local Similarity 33.6%; Pred. No. 1,6e-37;
 Matches 187; Conservative 87; Mismatches 185; Indels 97; Gaps 22;

36 OGGYKKEFKVT-VEKYKCKCHLVLCSPKQTCGHRPESGMAALLSSSPKCTAC-QE 93
 16 QPGSKTLGCKLEAKKACACRNVLRPPQACGHRGSCFLASITLSSGPQNCACVHE 75
 94 SIYADKY- - - - - FDNCKREIILAIQICRNESSGCAEQLMGLVHLKNDCHFEEL 145
 76 GYEGEGISILESSAFEDNARREVELPAVC--PSDGCYTK- - - - - TLKYEES-CHEGRC 129
 146 PCVR- - - - - PDCKEYLRDLRDHVEKACKYREATCSHCKSQVPMIALOKHEDTDCPVVVS 202
 130 PLMLTEPCACGGLVRLGKERHLEHECEPERSLSCRHRAPCCADVAAHHEV-CRPFPLT 188
 203 CPHKCSVOTLRLSELSEALISECVNAPSTCSFKRGCV--FQGTNQOIKAHBASAVOHVN 260
 189 C-DGGGKKRIPREFQDHYKTCGKCRVCRPHAIQCLETVGEKQO--EHEVQWLRREHLA 245
 261 LKEMNSLEKK- - - - - VSLIQN-ESVEKAKKSQSLAHNDCSEFEIEIEOKMLR 309
 246 ML--LSSVLEAKPILGDQSHASELJORCESLEKRTA--TEENIVCVINREVER- - - - - 295
 310 NNESTKLHQRVIDSOAEKLEKKEIRPFQNMWEADSMSSVSYSIQRNRYTELESVDKS 369
 296 - - - - - VAMTAELCS- - - - - RQHRLDQD- - - - - KIBALSSKYQOLE- - - - - 325
 370 - - - - - GOVARTGTLLESQLSRHDQMLSVHDIRLADNDLGFQVLETASYNGVLIWKIRDKRRKQ 429
 326- - - - - NSIGL- - - - - KDLAMADLEQKVRPFQACGHRGSCFLASITLRLKQ 366

430 EAVNGKTLISXQSPFYNGFYKMKCAVYILNDGNGKTHLSFEVYIMRGEYDALLPPE 489
 367 EAVAGRIPATFSPAYTSRIGYKNCRLIYINGDGTGTHLSFEVYVMPGNDALLRWF 426
 490 KQKVTLMMDQSSRRHLGDAFKPDPNSSSFKKPTGSMNINASCPEVAQVLE-NGTYI 548
 427 NQKVTLMMDQ-NNREHVIDAFRDPVYSSSFQRPVNDMNASGCPLECFVSKNEANSYV 485
 549 KDDTIFIKYVDTSDL 564
 486 RDAIFIKALVDLTEL 501

RESULT 5
 ID TRAF_HUMAN STANDARD; PRT; 416 AA.
 AC Q13077;
 DT 15-FEB-2000 (rel. 39, Created)
 DT 15-FEB-2000 (rel. 39, Last sequence update)
 DT 15-FEB-2000 (rel. 39, Last annotation update)
 DE TNF RECEPTOR ASSOCIATED FACTOR 1 (TRAF1) (ERSTEIN-BARR VIRUS-INDUCED
 DE PROTEIN 6).
 GN TRAF1 OR EB16.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LYMPHOMA;
 RX MEDLINE: 95163092.
 RX Mostafaei G., Birkenbach M., Yalamanchili R., VanArsdale T., Ware C.,
 RA Kleif E.,
 RT "The Epstein-Barr virus transforming protein LMP1 engages signaling
 RT proteins for the tumor necrosis factor receptor family."
 RT Cell 80:389-399(1995).
 RL -1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN
 CC OF THE 75 KDA TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2). THIS
 CC -1- SUBUNIT: HOMODIMER OR HETERODIMER OF TRAF1 AND TRAF2. THIS
 CC HETEROCOMPLEX CAN BIND TO THE N-TERMINAL OF INHIBITOR OF APOPTOSIS
 CC PROTEINS 1 AND 2 (IAPs), TO RECRUIT THEM TO THE TUMOR NECROSIS
 CC FACTOR RECEPTOR 2 (TNFR2).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: CONTAINS A MATH/TRAF DOMAIN.
 CC
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 CC
 CC EMBL: U19261; AAA62309.1; -
 CC DR MIM: 601711;
 CC DR PFM: PF00917; MATH; 1.
 CC DR COILED COIL 182 264 COILED COIL (POTENTIAL).
 CC FT DOMAIN 269 354 MATH/TRAF.
 CC FT DOMAIN 416 4613 MW; A956A123AA0D284A CRC64;
 CC
 CC SEQUENCE 416 AA; 46163 MW; A956A123AA0D284A CRC64;
 SQ

Query Match 21.2%; Score 637.5; DB 1; Length 416;
 Best Local Similarity 35.3%; Pred. No. 9,9e-32;
 Matches 164; Conservative 72; Mismatches 126; Indels 103; Gaps 17;

137 KNDCHFEELPCYRPPCKEKYLRKDLRDHVEKACKYREATCSHCKSQVPMIALOKHEDTDC 196
 15 ENEFPFGCPPTVQDPKPE- - - - - RALCCAGCJSENP- - - - - RRGEOJIC 54
 197 PCVVVSCPHKCSVQTL- - - - - LRSLSAHLSECVNAPSTCSFKRGCVFQGTNQOIK 248
 55 P- - - - - KNGEDLOSISPSGRILTOEKAH-PEVAEAGIGCFPAGVGCSFKNSPSVQ 105

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OM protein - protein search, using sw model

Run on: September 2, 2000, 10:20:59 ; Search time 54.15 Seconds
(without alignments)
725.992 Million cell updates/sec

Title: US-09-224-556-2
Perfect score: 3005
Sequence: 1 MESSKMDSPGALQTNPLK.....IKDDTIFIKVIYDSDLPDP 567

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Database: 225878 seqs, 69334122 residues
Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organellar:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2980.5	99.2	568	4	Q13114
2	2859	95.1	567	11	Q60803
3	1244	41.4	558	11	P70191
4	1244	41.4	558	11	Q61480
5	1182	39.3	557	4	O00463
6	822.5	27.4	508	11	O54896
7	735.5	24.5	501	4	Q12933
8	637.5	21.2	416	4	Q13077
9	554.5	18.5	522	4	Q9Y4K3
10	534	18.4	470	4	Q14848
11	537.5	17.9	530	11	P70196
12	520	17.3	470	11	Q61382
13	519	17.3	509	5	O62248
14	506.5	16.9	486	5	O9XYR0
15	260.5	8.7	463	5	O9XYQ9
16	208	6.9	198	4	O75615
17	169	5.6	528	13	Q91885
18	164	5.5	891	4	O9Y2K3
19	159	5.3	852	2	Q9X1X1

20	156.5	5.2	808	4	Q15083	Q15083 homo sapien
21	156	5.2	1816	11	O88785	O88785 mus musculu
22	152	5.1	1816	11	P97927	P97927 mus musculu
23	151.5	5.0	634	11	O61510	O61510 mus musculu
24	150.5	5.0	1676	10	O23332	O23332 arabidopsis
25	149	5.0	919	1	O9YFZ1	O9YFZ1 aeropyrum p
26	147.5	4.9	1005	1	O58718	O58718 methanococ
27	147	4.9	609	13	Q92021	Q92021 xenopus lae
28	146.5	4.9	610	13	Q91431	Q91431 xenopus lae
29	145	4.8	713	13	O9YHD6	O9YHD6 rana catesb
30	145	4.8	1300	4	Q13999	Q13999 homo sapien
31	144.5	4.8	846	4	O75130	O75130 homo sapien
32	144	4.8	1364	13	Q90631	Q90631 gallus gall
33	143	4.8	1577	5	O20795	O20795 caenorhabd
34	142.5	4.7	476	13	Q91940	Q91940 xiphophorus
35	142.5	4.7	2253	13	P70012	P70012 xenopus lae
36	142	4.7	412	5	O16684	O16684 caenorhabd
37	142	4.7	1356	4	Q14707	Q14707 homo sapien
38	142	4.7	1583	4	O15045	O15045 homo sapien
39	141	4.7	2230	4	Q13439	Q13439 homo sapien
40	140	4.7	879	1	O58687	O58687 pyrococcus
41	139.5	4.6	3113	4	Q13246	Q13246 homo sapien
42	139	4.6	1012	4	O75665	O75665 homo sapien
43	139	4.6	1218	11	O70365	O70365 mus musculu
44	138	4.6	1690	5	O44929	O44929 drosophila
45	137.5	4.6	1974	5	Q21000	Q21000 caenorhabd

ALIGNMENTS

RESULT 1

ID Q13114 PRELIMINARY; PRT; 568 AA.

AC Q13114; Q13076; Q13947; Q12990;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)

DE TNF RECEPTOR ASSOCIATED FACTOR 3 (CD40 RECEPTOR ASSOCIATED FACTOR 1) (CRAFT) (LMP1 ASSOCIATED PROTEIN) (LAP1).

GN TNF3 OR CRAFT OR CAP-1 OR CD40BP.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 95184010.

RA CHENG G., CLEARY A.M., YE Z.S., HONG D.I., LEDERMAN S., BALTIMORE D., "Involvement of CRAFT, a relative of TRAF, in CD40 signaling.";

RT Science 267:1494-1498(1995).

RN [2]

RP SEQUENCE FROM H.A., AND CHARACTERIZATION.

RX TISSUE-LYMPHOMA;

RA MEDLINE; 95163092.

RA MOSTALOS G., BIRKENBACH M., YALAMANCHILI R., VANARSDALE T., WARE C., KIERP E., "The Epstein-Barr virus transforming protein LMP1 engages signaling proteins for the tumor necrosis factor receptor family.";

RT Cell 80:389-399(1995).

RN [3]

RP SEQUENCE FROM N.A.

RX TISSUE-FETAL BRAIN;

RA MEDLINE; 95129692.

RA SATO T., IRIE S., REED J.C., "A novel member of the TRAF family of putative signal transducing proteins binds to the cytosolic domain of CD40.";

RT FEBS Lett. 358:113-118(1995).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE; 95073988.

RA HU H.M., O'ROURKE K., BOGUSKI M.S., DIXIT V.M., "A novel RING finger protein interacts with the cytoplasmic domain of CD40.";

RL J. Biol. Chem. 269:30069-30072(1994).
 CC -1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN
 CC OF THE 75 KD TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2). ALSO BINDS
 CC TO CD40 AND THE LYMPHOTOXIN-BETA RECEPTOR.
 CC -1- FUNCTION: MAY BE INVOLVED IN GASTRULATION (BY SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER OR HETERODIMER WITH OTHER TNF RECEPTOR
 CC ASSOCIATED FACTORS (POTENTIAL).
 CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
 DR EMBL: U21092; AAC50112.1; -
 DR EMBL: U19260; AAA65732.1; -
 DR EMBL: U138509; AAA68195.1; -
 DR EMBL: U15637; AAA56753.1; -
 DR MIM: 601896; -
 DR PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
 DR PFAM: PF00917; MATH; 1.
 DR PFAM: PF00097; zf-C3HC4; 1.
 KW Zinc-finger; Coiled coil.
 FT ZN_FING 68 77 C3HC4-TYPE.
 FT DOMAIN 267 338 COILED COIL (POTENTIAL).
 FT CONFLICT 129 129 T -> M (IN REF. 2 AND 4).
 FT CONFLICT 134 134 MISSING (IN REF. 4).
 FT CONFLICT 218 242 MISSING (IN REF. 3).
 FT CONFLICT 339 339 P -> S (IN REF. 3).
 FT CONFLICT 405 405 R -> G (IN REF. 4).
 SQ SEQUENCE 568 AA; 64459 MW; 77A8CDB8 CRC32;

Query Match 99.2%; Score 2980.5; DB 4; Length 568;
 Best Local Similarity 99.5%; Pred. No. 2,3e-181;
 Matches 565; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 MESSKMDSPGALQTNPLKLTDRSAGTPVFEVDEGGYKEKFKYVEDKXKCKCHLV 60
 DB 1 MESSKMDSPGALQTNPLKLTDRSAGTPVFEVDEGGYKEKFKYVEDKXKCKCHLV 60
 QY 61 CSPRQTCGHRFCSCMAALLSSSPCTACQESIVADKYKNDCKCKREILALQYCRNE 120
 DB 61 CSPRQTCGHRFCSCMAALLSSSPCTACQESIVADKYKNDCKCKREILALQYCRNE 120
 QY 121 SRGCAEOLMGH-LVHLKNDCHFEELPCVRPDECKEYLRKDLRDHVHAKCYRREATCSHC 179
 DB 121 SRGCAEOLMGH-LVHLKNDCHFEELPCVRPDECKEYLRKDLRDHVHAKCYRREATCSHC 180
 QY 180 KSGVPMIALOKHEDTDCPCVAVVSCPHKCSVOTLLRSELSAHLSVCVNA PSTCSFKRYGCV 239
 DB 181 KSGVPMIALOKHEDTDCPCVAVVSCPHKCSVOTLLRSELSAHLSVCVNA PSTCSFKRYGCV 240
 QY 240 FQGNQOIKAEHSAVQHVHLKEMSNLSLEKYSILQNESVEKNKSIQSLHNOICSPFI 299
 DB 241 FQGNQOIKAEHSAVQHVHLKEMSNLSLEKYSILQNESVEKNKSIQSLHNOICSPFI 300
 QY 300 EIEROKEMLRNNEKILHLQFVIDSOAEKLELDKEIRPFQONNEADSMKSVESLQNR 359
 DB 301 EIEROKEMLRNNEKILHLQFVIDSOAEKLELDKEIRPFQONNEADSMKSVESLQNR 360
 QY 360 VTELESYDKSAGVARNGLLESQSLSRHDQMLSYHDIRLAMDGLFYVLETAASNGVLIW 419
 DB 361 VTELESYDKSAGVARNGLLESQSLSRHDQMLSYHDIRLAMDGLFYVLETAASNGVLIW 420
 QY 420 KIRYKRRKQAVVNGKTLSTYSOPFYGYEYKMKCARVLYLNGDGKGTSLSTLFFVIRG 479
 DB 421 KIRYKRRKQAVVNGKTLSTYSOPFYGYEYKMKCARVLYLNGDGKGTSLSTLFFVIRG 480
 QY 480 EYDALLPMPFKOKYTIMLMDQSSRRHLGDAFKDPNNSSEFKPTGENNIAAGCPVFAVQ 539
 DB 481 EYDALLPMPFKOKYTIMLMDQSSRRHLGDAFKDPNNSSEFKPTGENNIAAGCPVFAVQ 540
 QY 540 TVLENGYIKDDTIFIKYIVDTSLDLP 567
 DB 541 TVLENGYIKDDTIFIKYIVDTSLDLP 568

RESULT 2

060803
 ID 060803 PRELIMINARY; PRT: 567 AA.
 AC 060803; 062380;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
 DE TNF RECEPTOR ASSOCIATED FACTOR 3 (CD40 RECEPTOR ASSOCIATED FACTOR 1)
 DE (CRAFT) (TRAFFAMN).
 GN TRAF3 OR CRAFT OR TRAFAMN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 95184010.
 RA CHENG G., CLEARY A.M., YE Z., HONG D.I., LEDERMAN S., BALTIMORE D.;
 RT "Involvement of CRAFT, a relative of TRAF, in CD40 signaling.";
 RL Science 267:1494-1498(1995).
 RN [2]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RC STRAIN-C57BL/6J; TISSUE-BRAIN;
 RX MEDLINE: 96299439.
 RA WANG X., BORNISLAEGER E.A., HAUB O., TOMIHARA-NEUBERGER C., LONBERG N.,
 RA DINILOS M.B., DISTECHE C.M., COPELAND N., GILBERT D.J., JENKINS N.A.,
 RA LACY E.;
 RT "A candidate gene for the amniotless gastrulation stage mouse mutation
 RT encodes a TRAF-related protein.";
 RL Dev. Biol. 177:274-290(1996).
 CC -1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN
 CC OF THE 75 KD TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2). ALSO BINDS
 CC TO CD40 AND THE LYMPHOTOXIN-BETA RECEPTOR (BY SIMILARITY).
 CC -1- FUNCTION: MAY BE INVOLVED IN GASTRULATION.
 CC -1- SUBUNIT: HOMODIMER OR HETERODIMER WITH OTHER TNF RECEPTOR
 CC ASSOCIATED FACTORS (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: (IN ADULT), HIGHEST IN BRAIN. ALSO FOUND IN
 CC KIDNEY, HEART, THYMUS, SPLEEN, LUNG, MUSCLE, TESTIS AND OVARY. NOT
 CC FOUND IN LIVER.
 CC -1- DEVELOPMENTAL STAGE: IN THE EMBRYO, EXPRESSED FROM 6.5. HIGHEST
 CC LEVELS FOUND BETWEEN E11.5 AND E13.5. AT LATE STAGES OF GESTATION,
 CC FROM E14.5, ONLY LOW LEVELS ARE DETECTED.
 CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
 DR EMBL: U21050; AAC52175.1; -
 DR EMBL: U33840; AAC52710.1; -
 DR MGD: MGI:108041; Traf3.
 DR PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
 DR PFAM: PF00917; MATH; 1.
 DR PFAM: PF00097; zf-C3HC4; 1.
 KW Zinc-finger; Coiled coil.
 FT ZN_FING 67 76 C3HC4-TYPE.
 FT DOMAIN 266 337 COILED COIL (POTENTIAL).
 FT CONFLICT 72 73 CE -> WQ (IN REF. 2).
 FT CONFLICT 390 390 T -> M (IN REF. 2).
 SQ SEQUENCE 567 AA; 64263 MW; F85A30F3 CRC32;

Query Match 95.1%; Score 2859; DB 11; Length 567;
 Best Local Similarity 95.6%; Pred. No. 1.1e-173;
 Matches 545; Conservative 7; Mismatches 16; Indels 2; Gaps 2;

QY 1 MESSKMDSPGALQTNPLKLTDRSAGTPVFEVDEGGYKEKFKYVEDKXKCKCHLV 60
 DB 1 MESSKMDSPGALQTNPLKLTDRSAGTPVFEVDEGGYKEKFKYVEDKXKCKCHLV 59
 QY 61 CSPRQTCGHRFCSCMAALLSSSPCTACQESIVADKYKNDCKCKREILALQYCRNE 120
 DB 60 CSPRQTCGHRFCSCMAALLSSSPCTACQESIVADKYKNDCKCKREILALQYCRNE 119
 QY 121 SRGCAEOLMGH-LVHLKNDCHFEELPCVRPDECKEYLRKDLRDHVHAKCYRREATCSHC 179
 DB 120 SRGCAEOLMGH-LVHLKNDCHFEELPCVRPDECKEYLRKDLRDHVHAKCYRREATCSHC 179
 QY 180 KSGVPMIALOKHEDTDCPCVAVVSCPHKCSVOTLLRSELSAHLSVCVNA PSTCSFKRYGCV 239
 DB 180 KSGVPMIALOKHEDTDCPCVAVVSCPHKCSVOTLLRSELSAHLSVCVNA PSTCSFKRYGCV 239

Db 180 KSGVPMIKLQKHEDTDCPVVSCPHKCSVQTLRLSELSEAHSECNAVAPSTCSFRRYGCV 239
QY 240 FQGINNOIKAHEASSAVQHVLLKEMNSLEKYSLLQNEVEKNKSIQSIHNOICSEI 299
Db 240 FQGINNOIKAHEASSAVQHVLLKEMNSLEKYSLLQNEVEKNKSIQSIHNOICSEI 299
QY 300 EIEKOKEMLRNNEKSIHLQVIDSQAELKELDKETIRPFQNMWEADSMKSVESLQNR 359
Db 300 EIEKOKEMLRNNEKSIHLQVIDSQAELKELDKETIRPFQNMWEADSMKSVESLQNR 359
QY 360 VTELESVDKSGQVARNVTGLLESQLSRHQDMLSVHDIRLADMGLFOYLETAASYNGVLW 419
Db 360 VTELESVDKSGQVARNVTGLLESQLSRHQDMLSVHDIRLADMGLFOYLETAASYNGVLW 419
QY 420 KIRYKRRKQAVNGKTLSTLSQPFYTGFGYKMCARYLNGDMGKTHLSLFVIMRG 479
Db 420 KIRYKRRKQAVNGKTLSTLSQPFYTGFGYKMCARYLNGDMGKTHLSLFVIMRG 479
QY 480 EYDALLPMPFROKQYTLMLMDGSSRRHLGDAFKPDPNSSFKPTGEMNINASGCPVEVYAO 539
Db 480 EYDALLPMPFROKQYTLMLMDGSSRRHLGDAFKPDPNSSFKPTGEMNINASGCPVEVYAO 539
QY 540 TVLENGTYIKDITFIKVIYDTSOLPDP 567
Db 540 TVLENGTYIKDITFIKVIYDTSOLPDP 567

RESULT 3
ID P70191 PRELIMINARY; PRT; 558 AA.
AC P70191;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE TRAF5.
GN TRAF5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96382484.
RA ISHIDA T., TOJO T., AOKI T., KOBAYASHI N., OHISHI T., WATANABE T.,
RA YAMAMOTO T., INOUE J.;
RT "TRAF5, a novel tumor necrosis factor receptor-associated factor
family protein, mediates CD40 signaling.";
PROC. Natl. Acad. Sci. U.S.A. 93:9437-9442(1996).
RT -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
EMBL; D83528; BA11942.1; -.
DR MGD; MGI:107548; Traf5.
DR PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
DR PFM; PFM0917; MATH; 1.
DR PFM; PFM0097; Zf-C3HC4; 1.
KM Zinc-finger.
SQ SEQUENCE 558 AA; 64145 MW; 43FCFDD4 CRC32;

Query Match 41.4%; Score 1244; DB 11; Length 558;
Best Local Similarity 42.7%; Pred. No. 2e-71;
Matches 243; Conservative 115; Mismatches 173; Indels 38; Gaps 12;
QY 22 HTDSAGRP-VFVPEOGG-----YKRFYKTVEDKCKCEKCHLVLCSPKQTEGCH 70
Db 3 HSEQAAVPCAFIRQNGNSISLDEPDTEYQFQLEERKCAFCHSVLNPHTGCGH 62
QY 71 RFCESCMAALIS-SSSPKTAQESIVKDKYKDNCKKREITAIQIYCRNRSRGAQOLM 129
Db 63 RFCQCCIRSLSELNSVPCIPVDKVIKQEVFKDNCKKREVLNHYCKN-APGCNARI 121
QY 130 LG-----HLVHLKNDCHFEELPCVPRDCKEYLRKDLRDHYKACKYREATSGHCKSQVPM 185
Db 122 LGRFDHLOH-----CSFOAVPCPNESCREAMLRKDVKEHLNAYCFRREKCLYCKRDIV 177

QY 186 IALQKHEDTDCPVVSCPHKCSVQTLRLSELSEAHSECNAVAPSTCSFRRYGCVFOGTNO 245
Db 178 TNLQDHEHNSCPRAIPVSCPNRC-VQITPRARVNHLYVCPAEDCCFPKHGCTYKVRKG 236
QY 246 QIKAHASSAVQHVLLKEMNSLEKYSLLQNEVEKNKSIQSIHNOICSEIEIEROK 305
Db 237 NLBHERAALQDHLVLLENKYQLEQRTSDLYQSLQEKESITQDLAETVKKFEKELQFT 296
QY 306 EMLRNNEKSIHLQVIDSQAELKELDKETIRPRQ--NWE---EADSMKSVESLQNR 359
Db 297 QMFGRNCTFJLNMV-ALTSHTDKGAWLEAQYROLQIYNOQPSRLDRLSDAIVSYKOR 355
QY 360 VTELESVDKSGQVARNVTGLLESQLSRHQDMLSVHDIRLADMGLFOYLETAASYNGVLW 419
Db 356 ITQLEASD-----QRLVLEGETSKDAHINIHKAQLNKNERFQLEGACYSKILW 408
QY 420 KIRYKRRKQAVNGKTLSTLSQPFYTGFGYKMCARYLNGDMGKTHLSLFVIMRG 479
Db 409 KVTDYRKRAVAGHIVSVSQPFYTSRGYRLCAVAYLNGDSGKTHLSLFVIMRG 468
QY 480 EYDALLPMPFROKQYTLMLMDGSSRRHLGDAFKPDPNSSFKPTGEMNINASGCPVEVYAO 539
Db 469 EFDLQMPYRQRYTLMLMDGSKRNHIVERFKADPNSSFKRPDGEKNINASGCPVEVYAO 528
QY 540 TVLEN--GTYIKDITFIKVIYDTSOLPDP 566
Db 529 STENSKNTYIKDITFLKVAVDLJLDED 557

RESULT 4
ID 061480 PRELIMINARY; PRT; 558 AA.
AC 061480;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE TRAF5.
GN TRAF5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96278943.
RA NAKANO H., OSHIMA H., CHUNG W., WILLIAMS-ABBOTT L., WARE C.F.,
RA YAGITA H., OKUMURA K.;
RT "TRAF5, an activator of NF-kappaB and putative signal transducer for
the lymphotoxin-beta receptor.";
J. Biol. Chem. 271:14661-14664(1996).
RT -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
CC EMBL; D78141; BA11218.1; -.
DR MGD; MGI:107548; Traf5.
DR PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
DR PFM; PFM0917; MATH; 1.
DR PFM; PFM0097; Zf-C3HC4; 1.
KM Zinc-finger.
SQ SEQUENCE 558 AA; 64154 MW; 910ACC60 CRC32;

Query Match 41.4%; Score 1244; DB 11; Length 558;
Best Local Similarity 41.3%; Pred. No. 2e-71;
Matches 241; Conservative 113; Mismatches 163; Indels 66; Gaps 11;
QY 22 HTDSAGRP-VFVPEOGG-----YKRFYKTVEDKCKCEKCHLVLCSPKQTEGCH 70
Db 3 HSEQAAVPCAFIRQNGNSISLDEPDTEYQFQLEERKCAFCHSVLNPHTGCGH 62
QY 71 RFCESCMAALIS-SSSPKTAQESIVKDKYKDNCKKREITAIQIYCRNRSRGAQOLM 129
Db 63 RFCQCCIRSLSELNSVPCIPVDKVIKQEVFKDNCKKREVLNHYCKN-APGCNARI 121
QY 130 LG-----HLVHLKNDCHFEELPCVPRDCKEYLRKDLRDHYKACKYREATSGHCKSQVPM 185

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DB 122 IGRQDHLQ----CSFOAVPCPNESCRAEMLRKDVKEHLASAYCFREBEKLYCKRDIIV 177
QY 186 IALOKHEDTQPCVAVSCPHKCSQVOTLLRSELASHLSCVNAFSTCSKRRGCVFOGNO 245
DB 178 TNLQDHEHNSCPAYVSCPNBC-VQTLPRAVNEHLVYCPAEODCPFKHCTVYKGRG 236
QY 246 QIRKHAESAAYVNLKEMNSLEKAVSLTQNSVEKNKSIOSLHNOICSEIEIEROK 305
DB 237 NLEHERAALQDHLVLEKRYOQLORISDLXOSLEQKESILQOLAELYKFEKELQFT 296
QY 306 EMLRNN-----ESKILHQRVIDSQAEKLEKDELKPRQNMEE 345
DB 297 QMFRNGFTLSNVQALSHTDKSAWLEAVHRLQIYNQPSRL-----D 341
QY 346 ADSKSSVESLQNRVTELESVDKSAQVARNLTGLLESQLSRHQMLSVHDIRLADMIDGF 405
DB 342 LRSILDVADSVKQRTQLEASD-----QKLVLEGETSKDHAINTHKQKLNKNERF 394
QY 406 QVLEFASINGVLYMKIRIDYKRRKQEAVMGKTLSTXQPFYTGFGYKMCARVYLNGDMG 465
DB 395 KQLEGACSGSLIMKVTYDQYRKREAVGHTVYSQPFYTSRCGYRLCABAYLNGDGG 454
QY 466 KGHLSLFTVIMRGEYDALLPMPFQKQVTLMLMDQSSRRHGLDAFKRDPNSSFKEFTG 525
DB 455 KGHLSLFTVIMRGEYDALLPMPFQKQVTLMLMDQSSRRHGLDAFKRDPNSSFKEFTG 514
QY 526 EMTASGCPVFAQVLEN--GYIKDPTIFKIVYDTSDDPD 566
DB 515 EMTASGCPVFAQVLEN--GYIKDPTIFKIVYDTSDDPD 557
RESULT 5
ID 000463 PRELIMINARY: PRT: 557 AA.
AC 000463:
DB 01-JUL-1997 (TIREMBLrel. 04, Created)
DB 01-NOV-1998 (TIREMBLrel. 08, Last sequence update)
DB 01-NOV-1999 (TIREMBLrel. 12, Last annotation update)
DE TRAF5 (TNF RECEPTOR ASSOCIATED FACTOR 5).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 98172745.
RA MITSUISHI S., FUJITA M., ISHIDA T., AZUMA S., KATO K., HIRAJI M.,
RA OTSUKA M., YAMAMOTO T., INOUE J.;
"Cloning and characterization of a cDNA encoding the human homolog of
tumor necrosis factor receptor-associated factor 5 (TRAF5).";
Genomics 207:135-140(1998).
RN [2]
RP SEQUENCE OF 20-557 FROM N.A.
RX MEDLINE: 97321041.
RA NAKANO H., SHINDO M., YAMADA K., YOSHIDA M.C., SANTEE S.M., WARE C.F.,
RA JENKINS N.A., GILBERT D.J., YAGITA H., COPELAND N.G., OKUMURA K.;
"Human TNF receptor-associated factor 5 (TRAF5): cDNA cloning,
expression and assignment of the TRAF5 gene to chromosome 1q32.";
Genomics 42:26-32(1997).
CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
DB EMBL: AB000509; BAAS262.1; -.
DB PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
DB PFM: PF00917; MATH; 1.
DB PFM: PF00097; zf-C3HC4; 1.
KW Zinc-finger.
SQ SEQUENCE 557 AA: 64405 MM; F4GCB2A CRC32;

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Query Match 39.3%; Score 1182; DB 4; Length 557;
 Best Local Similarity 41.6%; Pred. No. 1.7e-67;
 Matches .229; Conservative 121; Mismatches 181; Indels 20; Gaps 8;

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QY 25 RSAGTPVFEVDEGGYKKEFKYTVEDKCYCKCHLYLCSFKQTCGHRFCSCMAALLS-S 83
DB 17 QNSGNSISLDEPSEIEQFPERLEERYKCAFCSHVLNPGQJGHRFCCHLSLELN 76
QY 84 SSPKCTACQESIVADKYFKNNCKKREITLALQIYCRNESCABDQMLGHLVHKNDCHF 143
DB 77 TVPICPDKVEIYISQEFKQNCCKREYVNLVYCSN-APGCNKKVILGRYQDHLQCLFQ 135
QY 144 ELPCVRDCKEYLRKDLRDHVERACKYREATCSCKSQVPMIALQKHEDTQPCVAVSC 203
DB 136 PVQCSNCKREPVLRLKDLKEHLASQCFRREKLYCKKDVVAVINLQNHENLCEYVFC 195
QY 204 PHKCSVOTLRLSELASHLSCVNAFSTCSKRRGCVQGTNOQIKAHASAVQVNLK 263
DB 196 PNMCA-KITLKVDEHLAVCPPEADQCPKHGCAVTDKRRNLQDHEHSALEHMLVL 254
QY 264 EMSNLEKQVSLQNSVEKNKSIOSLHNOICSEIEIEROKEMLRNNSKILHLQVID 323
DB 255 EKNVQLEQISDLKSLQKESKIQOLAETIKRLEKFKQFAQLFGKNGSFLPNIQ-VFA 313
QY 324 SQAEKLEKELKIRPF-----RQNEBADSMSVESLQNRVTELESVDKSAQVARN 377
DB 314 SHDKSAWLEAVHQLQMVNQDQNKEDLPRIMEAVDVKOKITLLEND-----QRL 366
QY 378 GLLESQLSRHQMLSVHDIRLADMIDGFQVLEFASINGVLYMKIRIDYKRRKQEAVMGKTL 437
DB 367 AVLEETNKDPTIFKIVYDTSDDPD 426
QY 438 SLVSQPFYTGFGYKMCARVYLNGDMGKTHLSLFTVIMRGEYDALLPMPFQKQVTLML 497
DB 427 SIFQSFYTSRCGYRLCABAYLNGDGGSHLSLFTVIMRGEYDALLPMPFQKQVTLML 486
QY 498 MDQSSRRHGLDAFKRDPNSSFKEFTGEMNIAAGCPVFAQVLEN--GYIKDPTIF 555
DB 487 LDQ-SGKNIMETKPPDNSSSFKRPGEMNIAAGCPVFAHSLVKNKNAVDTLFL 545
QY 556 KYIVDTSDDPD 566
DB 546 KYAVDITLED 556
RESULT 6
ID 054896 PRELIMINARY: PRT: 508 AA.
AC 054896:
DB 01-JUN-1998 (TIREMBLrel. 06, Created)
DB 01-JUN-1998 (TIREMBLrel. 06, Last sequence update)
DB 01-NOV-1999 (TIREMBLrel. 12, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR ASSOCIATED FACTOR 2A.
GN TRAF2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6; TISSUE=KIDNEY;
RX MEDLINE: 98129826.
RA BRINK R., LODISH H.F.;
"Human TNF receptor-associated factor 2 (TRAF2),
inhibits TNF-mediated NF-kappaB activation.";
J. Biol. Chem. 273:4129-4134(1998).
CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
DB EMBL: AF027570; AAC53545.1; -.
DB PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
DB PFM: PF00917; MATH; 1.
DB PFM: PF00097; zf-C3HC4; 1.
KW Zinc-finger.
SQ SEQUENCE 508 AA: 56757 MM; 619B659E CRC32;

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Query Match 27.4%; Score 822.5; DB 11; Length 508;
 Best Local Similarity 33.6%; Pred. No. 8.6e-45;

Matches 199; Conservative 91; Mismatches 186; Indels 117; Gaps 21;

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OY 3 SSKKNDSSGALQTNPLKHLHDSAGTFFVPEQGYKEKFKPT-VEDKYKCKEHLVLC 61
Db 2 AAASVTSFSGSELELDP-----GFSKTLTGTLKAYLCKSACKNTLR 42
OY 62 SPKQTECGHRCFESCM-----ALLSSSPK-CTAC-----QESI---VADKFFKNC 105
Db 43 RPFQACGCHRCFCLTJSLRCASTLSSSGPNCACAYEGIEGISTLESSAFPDNA 102
OY 106 KRETLALQIYCRNESCQAELMGLHVLKNDCHFEELPCVR--PDCKEVLKRDLR 162
Db 103 ARREVESLPAYCPND--GCTMK---GTLKEYES--CHEGLCPFLTLECPACKGLVLSKE 156
OY 163 DHEVACCKYREATCSHCKSOVPMIALQKHEDTDCPCVYVSCPHKCSVQTLRSELSAHS 222
Db 157 HHTDECPKRSLSCHCRAPCSHVDLEVHYEY-CPKFPILT-C-DGCGKKRIPRETFQDHR 214
OY 223 ECYNAPSTCSFRRYCGVGTNOQIKAHBASAVOHVNLKEMNSLEKVS----- 274
Db 215 ACSKRCVLCRHTVYCCSEKVEIENLQDHELQRLREHLALL--LSSFLKQASPGTLNVOG 272
OY 275 --LQNESVERKKSIOSLHNOICSEIEIERQKEMLRNNSKILHLQRYIDSQAELKEL 332
Db 273 PELQRCQILBQK-IATFENIVCVLNREYER-----VAVTAACSGRQHL 316
OY 333 DKETRFQNMWEADSMKSSVESLQNRVTELESVDKSAGQVARTGLLESQLSRDQMS 392
Db 317 DOD-----KIEALSNKYQOLE-----RSIGL----- 337
OY 393 VHDRLADMGLFOYLETASVNGVLIMKIRDKRRKOEAVNMGTSLISQPEYTFGFK 452
Db 398 -KDLMAADLEQKVSLESTVDGVFTWKISDFTKRQENAVAGRTSLSPATYSTRYGK 396
OY 453 MCARYTLNGDGKNGKSTHSLFEVIRGEYDALPMPFKOKVITMLMDGSSRRHLGDAFK 512
Db 397 MCLARYTLNGDGTGRGTHLSLFEVYVVKGPNDALQMPFNQKVTMLLDH-NNREHYIDAFR 455
OY 513 PDPNSSFRRKPTGEMNIASGCPVFAQVYLE-NGTYIKDDTFFIVYDTSUL 564
Db 456 PDPVSSSFQRPVSDMNIASGCPVSKMEAKNSYVRDALFIRAYDLTGL 508

RESULT 7
OY 012933 PRELIMINARY; PRT: 501 AA.
OY 012933;
OY 01-NOV-1996 (TREMBLrel. 01, Created)
OY 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
OY 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
OY TUMOR NECROSIS FACTOR TYPE 2 RECEPTOR ASSOCIATED PROTEIN 3.
OY TRAP3.
OY Homo sapiens (Human).
OY Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OY Eutheria; Primates; Catarrhini; Homiidae; Homo.
OY [1]
OY SEQUENCE FROM N.A.
OY MEDLINE; 95366938.
OY SONG H.Y., DONNER D.B.;
OY ROTHE M., WONG S.C., HENZEL W.J., GOBDEL D.V.;
OY "A novel family of putative signal transducers associated with the
OY cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";
OY Cell 78:661-692(1994).
OY [3]
OY SEQUENCE FROM N.A.
OY SONG H.Y.;
OY Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.

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CC -I- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
DR EMBL: U12597; AA87706.1; -.
DR PROSITE; PS00518; ZINC_FINGER_C3HC4; 2.
DR PFWAM; PF00917; MATH; 1.
DR PFWAM; PF00097; ZI-C3HC4; 1.
DR Zinc-finger.
SQ SEQUENCE 501 AA; 55794 MW; 1C62BC1F CRC32;

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Query Match 24.58; Score 735.5; DB 4; Length 501;
 Best Local Similarity 33.68; Pred. No. 2,7e-39;
 Matches 187; Conservative 87; Mismatches 185; Indels 97; Gaps 22;

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OY 36 OGGEYKEKFKPT-VEDKYKCKEHLVLCSPKQTECGHRCFESCMALLSSSPKCTAC-QE 93
Db 16 QPFSKTLTGTLKAYLCKSACKNTLRPFQACGCHRCFCLTJSLRCASTLSSSGPNCACAYE 75
OY 94 SIYKRV-----FKDNCKRETLALQIYCRNESCQAELMGLHVLKNDCHFEEL 145
Db 76 GIEEGISILSSSAFPDNNARREVESLPAYC--PSDCTMK---GTLKEYES--CHEGRG 129
OY 146 PCVR--PDCKEVLKRDLRDHEVACCKYREATCSHCKSOVPMIALQKHEDTDCPCVYVS 202
Db 130 PLMTTECPACKGLVRLGKERHLEHECPERSLSCHRCRAPCCGADVKAHHEV-CPKFPILT 188
OY 203 CPHKCSVQTLRSELSAHLSCEYNAPSTCSFRRYCGV--FGTNOQIYAHNESAQVAVN 260
Db 189 C-DGCGKKRIPRETFQDHRVTKCGRCVPCRFHAGLCTLVEGEKQ--EHEQWMLREHLA 245
OY 261 LKEMNSLEKK-----VSLQN--ESYERKKSIOSLHNOICSEIEIERQKEMLR 309
Db 246 ML--LSSYLEAKPFLGDGSHAGSELLQRCESLEKTA--TFENIVCVLNREYER----- 295
OY 310 NNSKILHLQRYIDSQAELKELDKETRFQNMWEADSMKSSVESLQNRVTELESVDKS 369
Db 296 -----VAMTAACSGRQHL-----KIRALSSKYQOLE----- 325
OY 370 AGQVARTGLLESQLSRDQMSVHDRLADMGLFOYLETASVNGVLIMKIRDKRRKQ 429
Db 326 -----RSIGL-----KDLMAADLEQKVSLESTVDGVFTWKISDFTKRQENAVAGRTSLSPATYSTRYGK 366
OY 430 EAVNMGTSLISQPEYTFGFKMCARYTLNGDGKNGKSTHSLFEVIRGEYDALPMPF 489
Db 367 EAVNAGRIRALFSPATYSTRYGKMKCLRYTLNGDGTGRGTHLSLFEVYVVKGPNDALQMPFNQKVTMLLDH-NNREHYIDAFR 426
OY 490 KOKVITMLMDGSSRRHLGDAFKPDPNSSFRRKPTGEMNIASGCPVFAQVYLE-NGTYI 548
Db 427 NOKVITMLMDQ-NNREHYIDAFRDPVTSFQRPVSDMNIASGCPVSKMEAKNSYV 485
OY 549 KDDTFFIVYDTSUL 564
Db 486 RDDALFIRAYDLTGL 501

RESULT 8
OY 013077 PRELIMINARY; PRT: 416 AA.
OY 013077;
OY 01-NOV-1996 (TREMBLrel. 01, Created)
OY 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
OY 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
OY EPSTEIN-BARR VIRUS-INDUCED PROTEIN.
OY Homo sapiens (Human).
OY Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OY Eutheria; Primates; Catarrhini; Homiidae; Homo.
OY [1]
OY SEQUENCE FROM N.A.
OY TISSUE-LYMPHOID TUMOR;
OY MOSTALOS G., BIRKENBACH M., VALAMANCHILI R., VANASDALE T., WARE C.,
OY KIEFF E.;
OY Cell 0:0-0(0).
OY EMBL; U19261; AAA62309.1; -.
OY PFWAM; PF00917; MATH; 1.

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SEQUENCE 416 AA; 46163 MM; 760442EC CRC32;

Query Match 21.2%; Score 637.5; DB 4; Length 416;
Best Local Similarity 35.3%; Pred. No. 3.5e-33;
Matches 164; Conservative 72; Mismatches 126; Indels 103; Gaps 17;

137 KNDCHFEELPCVRPOCKEVLKDLRDHYEKACKREATCSHQVPMALQKHEDTDC 196
15 ENDFPGCPPTVCODPKEP-----RALCCAGCJSENP-----RNGEDDIC 54
197 PCVVASCPRKCSYQVL-----LRSLSAHLSECVNAPSTCSKRRKGCYVPGTNOQIK 248
55 P-----KCRGDELQGISPGSRRLTQKRAH-PEVAENGICCPAGVGCSEKSPQSVQ 105
249 AHEASSAVOHVNL-----KEMS-----NSLEKVSLLQ-NESEYKKSQ-SLH 291
106 EHEVTISQTSHLNLLGFMKQWKARLCCGLESQPMALQVLSLQAAVAVAGDLEVDCY 165
292 NOJCSFEIEIEROKEMLRNNEKILHLQVYIDSQAELKELDKETIRPFQNMHEADSKMS 351
166 RAPCS-----ESQEE-----LALQHEM--KEKILAELEKRLVF-----E 198
352 SVESLQNRVTELESVDKSAQVARNGLLESOLSRH-----DOMLSVHDIRLA 399
199 NIVAVLNKVE-----ASHLALATSIHQSDREIRILSEQRYVELQOTLAOKDQALG 251
400 DMDGFOVLETSYNGVLYMKIRIDYKRRKQDAVNGKTLISYQPTTGYGYKMCARVYL 459
252 KLEBSLRLEASPDGFEIMKRTVTRCHESACGRVTSLESPFYAKYKLCRLYL 311
460 NGDGMKGKTHLSLFVYMRGEYDALLPMPFKOKVTLMMDQSSRRHLDGAFKPPDNSS 519
312 NGDGGKRTKTHLSLFVYMRGEYDALLPMPFRNKVTPHLLQ--NREHAIADAFRDLSAS 370
520 FKPTGEMNIASGCPVFAQTVLEN--GTYIKDDTIFIKYIVDT 562
371 FQRPQSETNVAAGCLPFLPLSLQSPKHAAYKDDTMFKCIYETS 415

RESULT 9
OQYAK3 PRELIMINARY; PRT; 522 AA.
AC OQYAK3:
DC 01-NOV-1996 (TREMBLrel. 12, Created)
DT 01-NOV-1996 (TREMBLrel. 12, last sequence update)
DT 01-NOV-1996 (TREMBLrel. 12, last annotation update)
DE PUTATIVE INTERLEUKIN 1 SIGNAL TRANSDUCER.
EN TRAF6.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC [1]
RN SEQUENCE FROM N.A.
RP MEDLINE: 96434892.
RX CAO Z., XIONG J., TAKEUCHI M., KURAMA T., GOBDEL D.V.;
RA "TRAF6 is a signal transducer for interleukin-1";
RL Nature 383:443-446(1996).
CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
CC EMBL: U78798; AAB38751.1; .
DR PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
DR ZINC-finger.
KW ZINC-finger.
SEQUENCE 522 AA; 59573 MM; AE59362 CRC32;

Query Match 18.5%; Score 554.5; DB 4; Length 522;
Best Local Similarity 26.5%; Pred. No. 8.3e-28;
Matches 143; Conservative 101; Mismatches 200; Indels 95; Gaps 15;
32 FVPEQGGIKKFKVTKVEKCKECHKHLYLSPKRGESCSMALSSSPKCTAC 91
49 FMEELIQDYVDEPDPLESKYECPLCLMDLRAVQTPGHRCKKACIIKSINDAGHKCPVD 108

92 QESIVKDFVFNCCCKREITLALQYCNRESGCAEOLMGLHLYLKNDCHEELPCVRPD 151
109 NEILLNQLFQNFKAKEILSLAWKCPNE--GCLKNELNLEHDHACHCFALMDC--PQ 164
152 CEKVLKRDLDNHYEKACKREATCSHQVPMALQKHEDTDCPCVVASCPRKCSYQV 211
165 CQRPQKHINHLKDCPRQVSDNCAASMAPEDEKH--DQNCPLANYICEY-CNT-1 221
212 LRSLSAHLSECVNAPSTCSKRRKGCYVPGTNOQIKAHASSAVOHVNLKEMSLE 270
222 LIREQPMNYDDCPAPICPTFTFGCHERKQNRNHLRLQENTQSHRLAAYSL- 280
271 KAVSLQNSVEKNSISLHNOCSFEIEIEROKEMLRNNEKILHLQVYIDSQAELK 330
281 -----SVIPDSGIS---EVNRFQETIHQLEGRVLDHQRRELTAMETOSMYVS 328
331 ELDKETIRPFQNMHEADSKMSVSESLQNRVTELESVDKSAQVARNGLLESOLSRHDM 390
329 ELKRTIR-----TLEDKVABIEA----- 346
391 LSVHDIRLADMDIGFOVLETSYNGVLYMKIRIDY-----KRRQDAVNGKTLISYQPTT 446
347 -----QCCNGIYINKIGFNGHKLQCEEE--KPVYIHPGTYT 382
447 GYFGKRCARVYLN--GDGMKGKTHLSLFVYMRGEYDALLPMPFKOKVTLMMDQSS-- 503
383 GKPKYKLCMLHLQPLAORCAVYISLFVYTMQGEDSHLPWFQGTIKRLTIDSEAPV 442
504 RRLHGDFAKPPDNSSFKKPTGEMNIAS--GCPVFAQTVLENGTYIKDDTIFIKYIVDT 561
443 RQNHBEIMDARPELLAFQRTIPRNPFGVYTFMHEALRQETIKDDTILVRCVST 501

RESULT 10
OQ4848 PRELIMINARY; PRT; 470 AA.
AC OQ4848:
DC 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-NOV-1996 (TREMBLrel. 12, last annotation update)
DE CYSTEIN RICH DOMAIN ASSOCIATED TO RING AND TRAF PROTEIN.
GN MLN 62, CARL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC [1]
RN SEQUENCE FROM N.A.
RP TISSUE-BREAST DERIVED METASTATIC LYMPH NODE.
RC MEDLINE: 96039245.
RX TOMASETTO C., REGNIER C.H., MOOG-LUTZ C., MATTEI M.G., CHENARD M.P.,
RA LIDEREAU R., BASSET P., RIO M.C.;
RL "Identification of four novel human genes amplified and overexpressed
RT in breast carcinoma and localized to the q11-q21.3 region of
RT chromosome 17";
RL Genomics 28:367-376(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BREAST DERIVED METASTATIC LYMPH NODE;
RX MEDLINE: 96029665.
RX REGNIER C.H., TOMASETTO C., MOOG-LUTZ C., CHENARD M.P., WENDLING C.,
RA BASSET P., RIO M.C.;
RL "Presence of a new conserved domain in CARL, a novel member of the
RT tumor necrosis factor receptor-associated protein family, which is
RT expressed in breast carcinoma";
RL J. Biol. Chem. 270:25715-25721(1995).
CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
CC EMBL: X80200; CA556491.1; .
DR PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
DR PFAM: PF00917; MATH; 1.
DR PFAM: PF00097; ZF-C3HC4; 1.
KW ZINC-finger.
SEQUENCE 470 AA; 53443 MM; F3B78A90 CRC32;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 2, 2000, 09:02:02 : Search time 54.67 Seconds
(without alignments)
245.656 Million cell updates/sec

Title: US-09-224-556-2

Perfect score: 3005

Sequence: 1 MESSKKMDSPALQTNPLK.....IKDDIFIKYIVTSDLPDP 567

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Indexed: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2995	99.7	567	1 R99259	Full-length CD40 b
2	2986.5	99.4	568	1 W03146	IMPI associated pr
3	2980.5	99.2	568	1 W27431	Human CRAFI-a (TRA
4	2980.5	99.2	690	1 W27428	Human CRAFI-b (TRA
5	2820	93.8	543	1 W27432	Human CRAFI-1sotof
6	2820	93.8	665	1 W27433	Human CRAFI-1sotof
7	2804	93.3	543	1 R98833	CD40 associated pr
8	2652.5	88.3	516	1 W27436	Human CRAFI-b-1sot
9	2652.5	88.3	638	1 W27437	Human CRAFI-b-1sot
10	2646.5	88.1	512	1 W27434	Human CRAFI-1sotof
11	2646.5	88.1	634	1 W27435	Human CRAFI-b-1sot
12	2416	80.4	472	1 R98835	Human CRAFI-1sotof
13	1244	41.4	558	1 W29257	CD40 associated pr
14	1244	41.4	558	1 W29257	Murine TRAF5, a no
15	1182	39.3	557	1 W29258	Human TRAF5, a nov
16	1182	39.3	557	1 W27610	Human TRAF5, a nov
17	952	31.7	181	1 R98834	Human TRAF5, a nov
18	831	27.7	157	1 R98834	Human TRAF5, a nov
19	827	27.5	157	1 R98834	Human TRAF5, a nov
20	637.5	21.2	416	1 W03147	CD40 associated pr
21	629	20.9	409	1 R90577	Mouse TRAF2, Tunon
22	554.5	18.5	522	1 W32113	Epstein-Barr Induc
23	554	18.4	470	1 W25766	Mouse TRAF1, Tunon
24	145	4.8	1104	1 R94957	Tumour necrosis fa
25	140	4.7	3248	1 R99795	Human CART1, Genes
26	139.5	4.6	2482	1 R72826	NF-X1 DNA-binding
27	139.5	4.6	2482	1 W23996	Kinetochores protei
28	137	4.6	712	1 W80485	Human mtosin amin
29	136	4.5	712	1 R06471	Islet cell antihod
30	131.5	4.4	725	1 W39165	Delayed protein fr
31	130	4.3	606	1 R99673	Human RHAMM protei
32	128.5	4.3	419	1 W81073	Human RHAMM protei
33	128.5	4.3	582	1 W81077	Amino acid sequenc

34	128.5	4.3	582	1	R01364	Human protein with
35	128	4.3	1201	1	R90345	Drosophila sp. Cos
36	127.5	4.2	285	1	R82689	Shrimp tropomyosin
37	127	4.2	630	1	W39166	Mouse RHAMM protei
38	126.5	4.2	465	1	R78921	Human haemochromat
39	126	4.2	1863	1	R76641	BRCA1 protei
40	125.5	4.2	245	1	W59133	BRCA1 protei
41	125	4.2	478	1	R81503	Homo sapiens Tub I
42	125	4.2	481	1	R81492	BRCA1 mutant from
43	125	4.2	631	1	R99675	BRCA1 mutant from
44	125	4.2	671	1	R81504	RHAMM 1-2a isoform
45	125	4.2	734	1	R81506	BRCA1 mutant from

ALIGNMENTS

RESULT	ID	Score	Query Match	Length	ID	Description
1	R99259	2995	99.7	567	1 R99259	Full-length CD40 b
2	R99259	2986.5	99.4	568	1 W03146	IMPI associated pr
3	R99259	2980.5	99.2	568	1 W27431	Human CRAFI-a (TRA
4	R99259	2980.5	99.2	690	1 W27428	Human CRAFI-b (TRA
5	R99259	2820	93.8	543	1 W27432	Human CRAFI-1sotof
6	R99259	2820	93.8	665	1 W27433	Human CRAFI-1sotof
7	R99259	2804	93.3	543	1 R98833	CD40 associated pr
8	R99259	2652.5	88.3	516	1 W27436	Human CRAFI-b-1sot
9	R99259	2652.5	88.3	638	1 W27437	Human CRAFI-b-1sot
10	R99259	2646.5	88.1	512	1 W27434	Human CRAFI-1sotof
11	R99259	2646.5	88.1	634	1 W27435	Human CRAFI-b-1sot
12	R99259	2416	80.4	472	1 R98835	Human CRAFI-1sotof
13	R99259	1244	41.4	558	1 W29257	CD40 associated pr
14	R99259	1244	41.4	558	1 W29257	Murine TRAF5, a no
15	R99259	1182	39.3	557	1 W29258	Human TRAF5, a nov
16	R99259	1182	39.3	557	1 W27610	Human TRAF5, a nov
17	R99259	952	31.7	181	1 R98834	Human TRAF5, a nov
18	R99259	831	27.7	157	1 R98834	Human TRAF5, a nov
19	R99259	827	27.5	157	1 R98834	Human TRAF5, a nov
20	R99259	637.5	21.2	416	1 W03147	CD40 associated pr
21	R99259	629	20.9	409	1 R90577	Mouse TRAF2, Tunon
22	R99259	554.5	18.5	522	1 W32113	Epstein-Barr Induc
23	R99259	554	18.4	470	1 W25766	Mouse TRAF1, Tunon
24	R99259	145	4.8	1104	1 R94957	Tumour necrosis fa
25	R99259	140	4.7	3248	1 R99795	Human CART1, Genes
26	R99259	139.5	4.6	2482	1 R72826	NF-X1 DNA-binding
27	R99259	139.5	4.6	2482	1 W23996	Kinetochores protei
28	R99259	137	4.6	712	1 W80485	Human mtosin amin
29	R99259	136	4.5	712	1 R06471	Islet cell antihod
30	R99259	131.5	4.4	725	1 W39165	Delayed protein fr
31	R99259	130	4.3	606	1 R99673	Human RHAMM protei
32	R99259	128.5	4.3	419	1 W81073	Human RHAMM protei
33	R99259	128.5	4.3	582	1 W81077	Amino acid sequenc

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Db 181 SQVPMIALQKHEDTDCPCVAVVSCPHKCSVOTLLRSELSEAHLSSECYNAPSTCSFRKRGCV 240
QY 241 QGTNOQIKAEHASSAVOHVNLKEMNSLEKVSLLQNESVEKNKSISQSLHNOICSEIE 300
Db 241 QGTNOQIKAEHASSAVOHVNLKEMNSLEKVSLLQNESVEKNKSISQSLHNOICSEIE 300
QY 301 IERQKEMLRNNESKILHLQRYIDSQAELKELDEIRFRFONWEADSMKSSVESLQNRV 360
Db 301 IERQKEMLRNNESKILHLQRYIDSQAELKELDEIRFRFONWEADSMKSSVESLQNRV 360
QY 361 TELESVDKASAGVARNGLLESQLSRHDQMLSVHDIRLADMDLGFVLETASYNGVLIMK 420
Db 361 TELESVDKASAGVARNGLLESQLSRHDQMLSVHDIRLADMDLGFVLETASYNGVLIMK 420
QY 421 IRDYKRRKQEAVMGKTLISLQPPYTYGFGYKMCARYTLNDGDKGKTHLSLFFVIMRG 480
Db 421 IRDYKRRKQEAVMGKTLISLQPPYTYGFGYKMCARYTLNDGDKGKTHLSLFFVIMRG 480
QY 481 YDALLPPEFKOKVTLMDQSSRRHLGDAFKPDNPSSFRKPTGEMNIAAGCPVFAQT 540
Db 481 YDALLPPEFKOKVTLMDQSSRRHLGDAFKPDNPSSFRKPTGEMNIAAGCPVFAQT 540
QY 541 VLENGTYIKDDTIFIKVIYVDSLDLP 567
Db 541 VLENGTYIKDDTIFIKVIYVDSLDLP 567

RESULT 2
W03146
ID W03146 standard; Protein; 568 AA.
AC W03146;
DE 23-OCT-1996 (first entry)
KW LMPI associated protein LMPI.
KW LMPI; LMPI associated protein 1; latent infection membrane protein;
KW tumour necrosis factor receptor associated factor; TRAF;
KW signal transduction; TNF; TNFR; lymphoblast; tumorigenesis; AIDS;
KW Hodgkin's disease; Burkitt's lymphoma; nasopharyngeal carcinoma;
KW mononucleosis; Epstein-Barr virus; EBV; therapy.
OS Homo sapiens.
FH Location/Qualifiers
FT domain
FT 245..568
FT /label= LMPI-Binding_domain
FT 309..341
FT /label= Coiled_coil_domain
FT domain
FT 406..568
FT /label= Carboxy-terminal domain
PN W0620723-A1.
PD 11-JUL-1996.
PE 28-DEC-1995; U16980.
PF 30-DEC-1994; US-367540.
PG (RGHM ) BRIGHAM & WOMENS HOSPITAL.
PI (REGC ) UNIV CALIFORNIA.
PI Birkenbach M, Kaye KM, Kieff E, Mosialos G, Vanarsdale T;
PI Ware C;
PI MPI; 96-333765/33.
DR N-PSDB: T31273.
PT Compounds and methods for controlling TRAF-mediated signals - by
PT modulating interactions between Epstein Barr virus encoded proteins
PT LMPI, LMPI, TNF, TNFR to inhibit lymphoblast growth and
PT tumorigenesis.
PS Claim 74; Page 58-60; 87pp; English.
CC A novel human B-cell protein (W03146), termed LMPI associated protein
CC 1 or LMPI, strongly associates with the cytoplasmic C-terminal domain
CC (W03148) of Epstein-Barr virus (EBV) latent infection transformed cell
CC growth. LMPI is related to murine tumour necrosis factor receptor
CC 1 (LMPI1), a domain that is stringently required for transformed cell
CC growth. LMPI appears to be the human homologue of murine TRAF1. LMPI
CC EBV6, appears to be the human homologue of murine TRAF1. LMPI
CC polypeptides, esp. the LMPI binding domain, coiled coil domain and
CC C-terminal domain can be used to inhibit LMPI-TRAF interaction.
CC Such polypeptides, which may be obt. by recombinant means (see
CC also T31273) can be used to treat infection and control cell growth
CC of tumourigenesis associated with LMPI-encoding viruses, partic. EBV.

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SQ Sequence 568 AA:
Query Match 99.4%; Score 2986.5; DB 1; Length 568;
Best Local Similarity 99.6%; Pred. No. 3e-227;
Matches 566; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MESSKMDSPGALQNPPLKLTHTDSAGRPVFPVDDGGYKKEFVTVEDKYCEKCHLV 60
Db 1 MESSKMDSPGALQNPPLKLTHTDSAGRPVFPVDDGGYKKEFVTVEDKYCEKCHLV 60
QY 61 CSPKQTECHRCESCMALLSSSPKTAQCESIVKDKVFKNCCREITLQIYCRNE 120
Db 61 CSPKQTECHRCESCMALLSSSPKTAQCESIVKDKVFKNCCREITLQIYCRNE 120
QY 121 SRGCAQMLIGH-LVHLKNDCHFEELPCVRPDKKEVLRKLDLHVEKCKYREAFCSHC 179
Db 121 SRGCAQMLIGH-LVHLKNDCHFEELPCVRPDKKEVLRKLDLHVEKCKYREAFCSHC 180
QY 180 KSQVPMIALQKHEDTDCPCVAVVSCPHKCSVOTLLRSELSEAHLSSECYNAPSTCSFRKRGCV 239
Db 181 KSQVPMIALQKHEDTDCPCVAVVSCPHKCSVOTLLRSELSEAHLSSECYNAPSTCSFRKRGCV 240
QY 240 FQGTNOQIKAEHASSAVOHVNLKEMNSLEKVSLLQNESVEKNKSISQSLHNOICSEIE 299
Db 241 FQGTNOQIKAEHASSAVOHVNLKEMNSLEKVSLLQNESVEKNKSISQSLHNOICSEIE 300
QY 300 EIRQKEMLRNNESKILHLQRYIDSQAELKELDEIRFRFONWEADSMKSSVESLQNRV 359
Db 301 EIRQKEMLRNNESKILHLQRYIDSQAELKELDEIRFRFONWEADSMKSSVESLQNRV 360
QY 360 VTELESVDKASAGVARNGLLESQLSRHDQMLSVHDIRLADMDLGFVLETASYNGVLIM 419
Db 361 VTELESVDKASAGVARNGLLESQLSRHDQMLSVHDIRLADMDLGFVLETASYNGVLIM 420
QY 420 KIRDYKRRKQEAVMGKTLISLQPPYTYGFGYKMCARYTLNDGDKGKTHLSLFFVIMRG 479
Db 421 KIRDYKRRKQEAVMGKTLISLQPPYTYGFGYKMCARYTLNDGDKGKTHLSLFFVIMRG 480
QY 480 EYDALLPPEFKOKVTLMDQSSRRHLGDAFKPDNPSSFRKPTGEMNIAAGCPVFAQT 539
Db 481 EYDALLPPEFKOKVTLMDQSSRRHLGDAFKPDNPSSFRKPTGEMNIAAGCPVFAQT 540
QY 540 TVLENGTYIKDDTIFIKVIYVDSLDLP 567
Db 541 TVLENGTYIKDDTIFIKVIYVDSLDLP 568

RESULT 3
W27431
ID W27431 standard; Protein; 568 AA.
AC W27431;
DE 27-MAR-1998 (first entry)
KW Human CRAF1-a (TRAF-3-p55) polypeptide.
KW CD40 receptor associated factor 1; CRAF1-a; TRAF-3, p55; human;
KW CD40 mediated intracellular signalling; organ rejection; allergy;
KW hay fever; autoimmune disease; systemic lupus erythematosus;
KW rheumatoid arthritis; myasthenia gravis; Graves' disease;
KW idiopathic thrombocytopenia purpura; haemolytic anaemia;
KW diabetes mellitus; psoriasis; hyper immunoglobulin E syndrome;
KW apoplexis; Riecher's syndrome; spondyloarthritis; Lyme disease; HIV;
KW syphilis; tuberculosis; arthritis; scleroderma; pulmonary fibrosis;
KW pneumoconiosis; adult respiratory distress syndrome; pneumonia;
KW asbestosis; silicosis; Farmer's lung; hepatitis; cirrhosis;
KW atherosclerosis; multiple sclerosis; glomerulonephritis;
KW glomerulosclerosis; glomerulopathy; kidney disease; nephropathy;
KW endocarditis; leprosy; malaria; Goodpasture's disease;
KW Henoch-Schoenlein purpura; polyarteritis; multiple myeloma;
KW Wegener's granulomatosis; cryoglobulinemia;
KW Waldenstrom's macroglobulinemia; amyloidosis; Sjogren's syndrome;
KW AIDS; oesophageal dysmotility; inflammatory bowel disease;
KW bladder disease; Epstein-Barr virus; mononucleosis; B cell tumour;
KW Burkitt's lymphoma; nasopharyngeal carcinoma; pneumonia;

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FT      Region                               330, His-343 and Cys-347)"
FT      /note= "zinc finger 5 (Zn binding to Cys-354,
FT      Cys-361, His-373 and His-381"
FT      Binding_site                          16..19
FT      /note= "putative SH3 binding motif"
FT      Binding_site                          44..47
FT      /note= "putative SH3 binding motif"
FT      Binding_site                          103..110
FT      /note= "putative SH3 binding motif"
PN      W09734473-A1.
PD      25-SEP-1997.
PE      21-MAR-1997.
PR      18-SEP-1996; US-026584.
PR      21-MAR-1996; US-013820.
PR      01-MAY-1996; US-016826.
PR      01-MAY-1996; US-016659.
PA      (UYCO ) UNIV COLUMBIA NEW YORK.
PI      Cleary AM, Frank DM, Lederman S;
PI      WPI: 97-479907/44.
DR      N-PSDB; T90123.
CC      Protein comprising CRAF1-b domain capable of inhibiting CD40
CC      mediated cell activation - useful to treat conditions characterised
CC      by aberrant or unwanted level of CD40 mediated intracellular
CC      signalling
CC      Example 1: Fig 1A-C; 158pp; English.
CC      This polypeptide comprises a CRAF1 (TRAF-3) protein designated
CC      CRAF1-b or TRAF-3-p70 or p70 or CRAF1(p70) or TRAF-3(p70). It
CC      is encoded by exons 1-2 and 4-13 of the human CRAF gene (see
CC      W27432). A lower mol. wt. CRAF1, designated CRAF1a (see W27431), has
CC      also been identified, as well as isoforms p5 (see W27429), p15 (see
CC      W27430) and variants of CRAF-1a and CRAF-b (see W27432-37) that
CC      comprise different combinations of zinc fingers. CRAF1 peptides,
CC      comprising from 0-4 zinc finger domains, and nucleic acids encoding
CC      them, can be used to inhibit CD40 ligand activation of cells that
CC      express CD40 on their surface, particularly by introducing the
CC      nucleic acid molecule into the cells, useful to treat conditions
CC      characterised by an aberrant or unwanted level of CD40 mediated
CC      intracellular signalling, such as organ rejection, or a CD40
CC      dependent immune response in a subject receiving gene therapy. The
CC      condition may be an allergic response or an autoimmune response, or
CC      may be dependent on CD40 ligand-induced activation of epithelial
CC      cells, an inflammatory kidney disease, a smooth muscle cell-
CC      dependent disease, or a condition associated with Epstein-Barr
CC      virus.
CC      Sequence 690 AA:
QY      Query Match                      99.2%; Score 2980.5; DB 1; Length 690;
QY      Best Local Similarity 99.5%; Pred. No. 1.2e-226;
QY      Matches 565; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY      1 MESSKRMDSFGALQTNPPILKLTDRSAGTPVFPDGGKKEKFTVTEDEKICECHLYL 60
QY      123 MESSKRMDSFGALQTNPPILKLTDRSAGTPVFPDGGKKEKFTVTEDEKICECHLYL 182
QY      61 CSPKQTEGHRCESCMAALLSSSSPKTACQESTIVKQVFQDNCKKRIIALQIYCENR 120
QY      183 CSPKQTEGHRCESCMAALLSSSSPKTACQESTIVKQVFQDNCKKRIIALQIYCENR 242
QY      121 SRGCAEQLMLGH-LVHLKNDCHFEELPCVPRDCKEKVLRKLDLHVEKACKTREATCSHC 179
QY      243 SRGCAEQLMLGH-LVHLKNDCHFEELPCVPRDCKEKVLRKLDLHVEKACKTREATCSHC 302
QY      180 KSOVPMIALQKREDTDCPCVVVSCCHKSGVQTLNLSELSAHLSECVNAPSTCSFRYGCY 239
QY      303 KSOVPMIALQKREDTDCPCVVVSCCHKSGVQTLNLSELSAHLSECVNAPSTCSFRYGCY 362
QY      240 FQGTNOQIRAHASSAYOVNLLKEMSNLEKVSILQNESEKKNKSIGSLNQCISFEI 299
QY      363 FQGTNOQIRAHASSAYOVNLLKEMSNLEKVSILQNESEKKNKSIGSLNQCISFEI 422
QY      300 EIEROKEMLRNNSKILHLQRVIDSQAEKLELDKEIRPFQONWEADSMKSSVESLQNR 359

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DB      423 EIEROKEMLRNNSKILHLQRVIDSQAEKLELDKEIRPFQONWEADSMKSSVESLQNR 482
QY      360 VTELESYDKAGQAVARTGLLESQLSRHQOMLSVHDIRLADMDLGRQVETASYNLVW 419
DB      483 VTELESYDKAGQAVARTGLLESQLSRHQOMLSVHDIRLADMDLGRQVETASYNLVW 542
QY      420 KIRDYKRRQEAVMGKTLSTXQPFYTGFGYKCAKARVYLNGDMGKGTLSLFFVIMRG 479
DB      543 KIRDYKRRQEAVMGKTLSTXQPFYTGFGYKCAKARVYLNGDMGKGTLSLFFVIMRG 602
QY      480 EYDALLPMPKQVYTLMDQSSRRHLGDAFKDPDSSSFKKPTGEMNTIASGCPVFAQ 539
DB      603 EYDALLPMPKQVYTLMDQSSRRHLGDAFKDPDSSSFKKPTGEMNTIASGCPVFAQ 662
QY      540 TVLENGTYIKDDTLEFIVYDTSIDLPDP 567
DB      663 TVLENGTYIKDDTLEFIVYDTSIDLPDP 690

RESULT 5
W27432
ID      W27432 standard; Protein; 543 AA.
AC      W27432;
DT      27-MAR-1998 (first entry)
DE      Human CRAF1 isoform p55del19.
KW      CD40 receptor associated factor 1; CRAF1-a; TRAF-3; p55; human;
KW      CD40 mediated intracellular signalling; organ rejection; allergy;
KW      hay fever; autoimmune disease; systemic lupus erythematosus;
KW      rheumatoid arthritis; myasthenia gravis; Graves' disease;
KW      idiopathic thrombocytopenia purpura; haemolytic anaemia;
KW      diabetes mellitus; psoriasis; hyper immunoglobulin E syndrome;
KW      apoptosis; Rietter's syndrome; spondyloarthritis; Lyme disease; HIV;
KW      syphilis; tuberculosis; arthritis; scleroderma; pulmonary fibrosis;
KW      pneumococcosis; adult respiratory distress syndrome; pneumonitis;
KW      asbestosis; silicosis; Farmer's lung; hepatitis; cirrhosis;
KW      atherosclerosis; multiple sclerosis; glomerulonephritis;
KW      glomerulosclerosis; glomerulopathy; kidney disease; nephropathy;
KW      endocarditis; leprosy; malaria; Goodpasture's disease;
KW      Henoch-Schoenlein purpura; polyarteritis; multiple myeloma;
KW      Wegener's granulomatosis; cryoglobulinemia;
KW      Waldenstrom's macroglobulinemia; amyloidosis; Sjogren's syndrome;
KW      AIDS; oesophageal dysmotility; inflammatory bowel disease;
KW      bladder disease; Epstein-Barr virus; mononucleosis; B cell tumour;
KW      Burkitt's lymphoma; nasopharyngeal carcinoma; pneumonia;
KW      gene therapy; diagnosis.
OS      Homo sapiens.
FH      Key
FT      Region                               Location/Qualifiers
FT      /note= "zinc finger 1 (Zn binding to Cys-117,
FT      Cys-124, His-136 and Cys-141)"
FT      Region                               148..170
FT      /note= "zinc finger 2 (zinc binding to Cys-148,
FT      Cys-153, His-165 and Cys-170)"
FT      Region                               177..197
FT      /note= "zinc finger 3 (Zn binding to Cys-177,
FT      Cys-180, His-192 and Cys-197)"
PN      W09734473-A1.
PD      25-SEP-1997.
PE      21-MAR-1997.
PR      18-SEP-1996; US-026584.
PR      21-MAR-1996; US-013820.
PR      01-MAY-1996; US-016826.
PR      01-MAY-1996; US-016659.
PA      (UYCO ) UNIV COLUMBIA NEW YORK.
PI      Cleary AM, Frank DM, Lederman S;
PI      WPI: 97-479907/44.
DR      N-PSDB; T90123.
CC      Protein comprising CRAF1-b domain capable of inhibiting CD40
CC      mediated cell activation - useful to treat conditions characterised
CC      by aberrant or unwanted level of CD40 mediated intracellular
CC      signalling
CC      Example 1: Fig 1D-C; 158pp; English.

```

CC This polypeptide comprises a CRAF1 (TRAF-3) isoform designated
 CC p53del9. It is encoded by exons 4-8 and 10-13 of the human CRAF
 CC gene (see T90123) and arises by alternative splicing of the
 CC transcript for CRAF1-a (see W27431), a signalling protein that
 CC interacts with the cytoplasmic tail of B cell surface molecule CD40
 CC and which mediates a variety of T-dependent effects on B cell
 CC activation and differentiation. A higher mol.wt. CRAF1, designated
 CC CRAF1b (see W27428), has also been identified, as well as isoforms
 CC p5 (see W27429), p15 (see W27430) and variants of CRAF-1a and
 CC CRAF-b (see W27432-37) that comprise different combinations of 5
 CC zinc fingers. CRAF1 peptides, comprising from 0-4 zinc finger
 CC domains, and nucleic acids encoding them, can be used to inhibit
 CC CD40 ligand activation of cells that express CD40 on their surface,
 CC particularly by introducing a nucleic acid molecule into the cells,
 CC and used to treat conditions characterised by an aberrant or
 CC unwanted level of CD40 mediated intracellular signalling, such as
 CC organ rejection, or a CD40 dependent immune response in a subject
 CC receiving gene therapy. The condition may be an allergic response
 CC or an autoimmune response, or may be dependent on CD40 ligand-
 CC induced activation of epithelial cells, an inflammatory kidney
 CC disease, a smooth muscle cell-dependent disease, or a condition
 CC associated with Epstein-Barr virus.
 CC Sequence 543 AA:

Query Match 93.8%; Score 2820; DB 1; Length 543;
 Best Local Similarity 95.1%; Pred. No. 3.7e-214;
 Matches 540; Conservative 0; Mismatches 2; Indels 26; Gaps 2;

QY 1 MESSKKMDSGALQTNPKLHTDRSAGTPFVPEQGGYKKEFKVTEVDKYCEKCHLV 60
 DB 1 MESSKKMDSGALQTNPKLHTDRSAGTPFVPEQGGYKKEFKVTEVDKYCEKCHLV 60
 QY 61 CSPKTEGHRCESCMALLSSSSPKACQESTYKDKVFNDCCKRITLALQTYCRNE 120
 DB 61 CSPKTEGHRCESCMALLSSSSPKACQESTYKDKVFNDCCKRITLALQTYCRNE 120
 QY 121 SRGCAEQMLTGH-LVHLKNDCHFEELPCVRPCKEKVLRKDLRDHYEAKCKREATCSHC 179
 DB 121 SRGCAEQMLTGH-LVHLKNDCHFEELPCVRPCKEKVLRKDLRDHYEAKCKREATCSHC 180
 QY 180 KSQVPMALQKHEDTDCPCVVVSCPHKCSVQTLNSELVAHLSECVNAPSTCSFRYGCY 239
 DB 180 KSQVPMALQKHEDTDCPCVVVSCPHKCSVQTLNSELVAHLSECVNAPSTCSFRYGCY 239
 QY 181 KSQVPMALQKHEDTDCPCVVVSCPHKCSVQTLNSELVAHLSECVNAPSTCSFRYGCY 217
 DB 181 KSQVPMALQKHEDTDCPCVVVSCPHKCSVQTLNSELVAHLSECVNAPSTCSFRYGCY 217
 QY 240 FQGTNOQIKAHASSAVQHVNLKEMSNLSLEKVSILQNESYEKKNSIOSLNOICSPFI 299
 DB 240 FQGTNOQIKAHASSAVQHVNLKEMSNLSLEKVSILQNESYEKKNSIOSLNOICSPFI 299
 QY 218 --GTNOQIKAHASSAVQHVNLKEMSNLSLEKVSILQNESYEKKNSIOSLNOICSPFI 275
 DB 218 --GTNOQIKAHASSAVQHVNLKEMSNLSLEKVSILQNESYEKKNSIOSLNOICSPFI 275
 QY 300 ETEROKEMLRNNEKILHLQRYIDSOAEKLELDEIRPFQNMWEPADSMKSSVSLONR 359
 DB 300 ETEROKEMLRNNEKILHLQRYIDSOAEKLELDEIRPFQNMWEPADSMKSSVSLONR 359
 QY 276 ETEROKEMLRNNEKILHLQRYIDSOAEKLELDEIRPFQNMWEPADSMKSSVSLONR 335
 DB 276 ETEROKEMLRNNEKILHLQRYIDSOAEKLELDEIRPFQNMWEPADSMKSSVSLONR 335
 QY 360 VTELESVDKSAQVARNLTGLSOLSRHDOMLSVDHRLADMDLFOVLETSYNGVLIM 419
 DB 360 VTELESVDKSAQVARNLTGLSOLSRHDOMLSVDHRLADMDLFOVLETSYNGVLIM 419
 QY 336 VTELESVDKSAQVARNLTGLSOLSRHDOMLSVDHRLADMDLFOVLETSYNGVLIM 395
 DB 336 VTELESVDKSAQVARNLTGLSOLSRHDOMLSVDHRLADMDLFOVLETSYNGVLIM 395
 QY 420 KIRDKRRKQEVNMGKTLSISQPFYTGFGYKMCARYLNDGKGKSHLSLFEVIMNG 479
 DB 420 KIRDKRRKQEVNMGKTLSISQPFYTGFGYKMCARYLNDGKGKSHLSLFEVIMNG 479
 QY 396 KIRDKRRKQEVNMGKTLSISQPFYTGFGYKMCARYLNDGKGKSHLSLFEVIMNG 455
 DB 396 KIRDKRRKQEVNMGKTLSISQPFYTGFGYKMCARYLNDGKGKSHLSLFEVIMNG 455
 QY 480 EYDALLPMPFKQVTLMDQSSRRHLGADAPKPPDNSSSFFKPTGEMNIASGCPVEVNO 539
 DB 480 EYDALLPMPFKQVTLMDQSSRRHLGADAPKPPDNSSSFFKPTGEMNIASGCPVEVNO 539
 QY 456 EYDALLPMPFKQVTLMDQSSRRHLGADAPKPPDNSSSFFKPTGEMNIASGCPVEVNO 515
 DB 456 EYDALLPMPFKQVTLMDQSSRRHLGADAPKPPDNSSSFFKPTGEMNIASGCPVEVNO 515
 QY 540 TVLENGYIKDDTIFIKYIVDTSDLPDP 567
 DB 540 TVLENGYIKDDTIFIKYIVDTSDLPDP 567
 QY 516 TVLENGYIKDDTIFIKYIVDTSDLPDP 543
 DB 516 TVLENGYIKDDTIFIKYIVDTSDLPDP 543

RESULT 6
 W27433
 ID W27433 standard; Protein: 665 AA.

AC W27433: (first entry)
 DT 27-MAR-1998
 DE Human CRAF1-b isoform p70del9.
 KW CD40 receptor associated factor 1; CRAF1-b; TRAF-3; p70; human;
 KW CD40 mediated intracellular signalling; organ rejection; allergy;
 KW hay fever; autoimmune disease; systemic lupus erythematosus;
 KW rheumatoid arthritis; myasthenia gravis; Graves' disease;
 KW idiopathic thrombocytopenia purpura; hemolytic anaemia;
 KW diabetes mellitus; psoriasis; hyper immunoglobulin E syndrome;
 KW apoptosis; Rieger's syndrome; spondylarthritis; Lyme disease; HIV;
 KW syphilis; tuberculosis; arthritis; scleroderma; pulmonary fibrosis;
 KW pneumoconiosis; adult respiratory distress syndrome; pneumonia;
 KW asbestosis; silicosis; Farmer's lung; hepatitis; cirrhosis;
 KW atherosclerosis; multiple sclerosis; glomerulonephritis;
 KW glomerulocystosis; glomerulopathy; kidney disease; nephropathy;
 KW endocarditis; leprosy; malaria; Goodpasture's disease;
 KW Henoch-Schoenlein purpura; polyarteritis; multiple myeloma;
 KW Wegener's granulomatosis; cryoglobulinemia;
 KW Waldenstrom's macroglobulinemia; amyloidosis; Sjogren's syndrome;
 KW AIDS; oesophageal dysmotility; inflammatory bowel disease;
 KW bladder disease; Epstein-Barr virus; mononucleosis; B cell tumour;
 KW Burkitt's lymphoma; nasopharyngeal carcinoma; pneumonia;
 KW gene therapy; diagnosis.
 OS Homo sapiens.
 FH Key
 FT 52. 122
 FT Domain
 FT /label="CRAF-b domain
 FT /note="Claim 1"
 FT Region
 FT 239. 263
 FT /note="zinc finger 1 (2n binding to Cys-239,
 FT Cys-246, His-258 and Cys-263)"
 FT Region
 FT 270. 292
 FT /note="zinc finger 2 (zinc binding to Cys-270,
 FT Cys-275, His-287 and Cys-292)"
 FT Region
 FT 299. 319
 FT /note="zinc finger 3 (2n binding to Cys-299,
 FT Cys-302, His-314 and Cys-319)"
 FT Binding_site
 FT 16. 19
 FT /note="putative SH3 binding motif"
 FT Binding_site
 FT 44. 47
 FT /note="putative SH3 binding motif"
 FT Binding_site
 FT 103. 110
 FT /note="putative SH3 binding motif"
 PN W09734473-A1.
 PD 25-SEP-1997.
 PF 21-MAR-1997; U05076.
 PR 18-SEP-1996; US-026584.
 PR 21-MAR-1996; US-013820.
 PR 01-MAY-1996; US-016626.
 PR 01-MAY-1996; US-016659.
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 PI Cleary AM, Frank DM, Lederman S;
 DR WPI; 97-47907/44.
 DR N-PSDB; T90123.
 PT Protein comprising CRAF1-b domain capable of inhibiting CD40
 PT mediated cell activation - useful to treat conditions characterised
 PT by aberrant or unwanted level of CD40 mediated intracellular
 PT signalling
 PS Example 1; Fig 1A-O; 158pp; English.
 CC This polypeptide comprises a CRAF1 (TRAF-3) protein designated
 CC p70del9 that is encoded by exons 1-2, 4-8 and 10-13 of the human
 CC CRAF gene (see T90123). Different isoforms (W27428-37) of CRAF1
 CC have been identified that arise from alternative splicing. CRAF1
 CC peptides comprising from 0-4 zinc finger domains, and nucleic acids
 CC encoding them, can be used to inhibit CD40 ligand activation of
 CC cells that express CD40 on their surface, particularly by
 CC introducing the nucleic acid molecule into the cells, and used to
 CC treat conditions characterised by an aberrant or unwanted level of
 CC CD40 mediated intracellular signalling, such as organ rejection, or
 CC CD40 dependent immune response in a subject receiving gene
 CC therapy. The condition may be an allergic response or an
 CC autoimmune response, or may be dependent on CD40 ligand-induced
 CC activation of epithelial cells, an inflammatory kidney disease, a

CC smooth muscle cell-dependent disease, or a condition associated
CC with Epstein-Barr virus.
SQ Sequence 665 AA;

Query Match 93.8%; Score 2820; DB 1; Length 665;
Best Local Similarity 95.1%; Pred. No. 4.9e-214;
Matches 540; Conservative 0; Mismatches 2; Indels 26; Gaps 2;

QY 1 MESSKMDSPGALQTNPKLHTDSAGTPVPPGQGGKEKFKVTEDEKCEKCHLV 60
DB 123 MESSKMDSPGALQTNPKLHTDSAGTPVPPGQGGKEKFKVTEDEKCEKCHLV 182
QY 61 CSPKQTECHRCESCMALLSSSPKCTACQESTYKDVFNCKCKREILAQIYCRNE 120
DB 183 CSPKQTECHRCESCMALLSSSPKCTACQESTYKDVFNCKCKREILAQIYCRNE 242
QY 121 SSGCAEQMLG-HLVHAKNDCHFEELPCVRPDCKEKYLKRDLDHYEKACKYREATCSHC 179
DB 243 SSGCAEQMLG-HLVHAKNDCHFEELPCVRPDCKEKYLKRDLDHYEKACKYREATCSHC 302
QY 180 KSOVPMIALQKHEDTDCPCVVVSCPHKCSVQTLNSELSAHLSECVNAPSTCSFKRYGCV 239
DB 303 KSOVPMIALQKHEDTDCPCVVVSCPHKCSVQTLNSELSAHLSECVNAPSTCSFKRYGCV 339
QY 240 FQGTNOQIAHASSAVQVHNLKEMNSLEKVSILLQNESVEKNSISLHNOICSEFI 299
DB 340 --GTNNOIAHASSAVQVHNLKEMNSLEKVSILLQNESVEKNSISLHNOICSEFI 397
QY 300 EIEROKEMLRNNEKSLHLOVYIDSOAEKLEKELKEIRPFQRMWEADSKSSVESLQNR 359
DB 398 EIEROKEMLRNNEKSLHLOVYIDSOAEKLEKELKEIRPFQRMWEADSKSSVESLQNR 457
QY 360 VTELESVDKSAGOVARNITGLLESQSLSRHDQMLSVHDIRLADMDLGFQVLETASYNGVLIM 419
DB 458 VTELESVDKSAGOVARNITGLLESQSLSRHDQMLSVHDIRLADMDLGFQVLETASYNGVLIM 517
QY 420 KIRDYRRKROEAVMGKTLISYQPFYTGFGYKMCARVYLNDGMRGTHLSLFEVIMRG 479
DB 518 KIRDYRRKROEAVMGKTLISYQPFYTGFGYKMCARVYLNDGMRGTHLSLFEVIMRG 577
QY 480 EYDALLPMPFKOKVITLMDQSSRRHLGDARFDPNNSSEFFKPTGEMNIAAGCPVFAVQ 539
DB 578 EYDALLPMPFKOKVITLMDQSSRRHLGDARFDPNNSSEFFKPTGEMNIAAGCPVFAVQ 637
QY 540 TVLENGTYIKDITFIKVIYDTSDDLDP 567
DB 638 TVLENGTYIKDITFIKVIYDTSDDLDP 665

RESULT 7
R98833
ID R98833 standard; Protein: 543 AA.
AC R98833;
DE 23-MAR-1998 (first entry)
CD40 associated protein: CAP-1.
KM CD40 associated protein: CAP; agonist; antagonist; gene therapy;
OS cell proliferation; treatment; cancer; autoimmune disease.
KW Homo sapiens.
FT Domain Location/Qualifiers
FT 53..91
FT /note= "RING finger domain"
FT 117..141
FT /note= "Zinc finger domain 1"
FT 148..170
FT /note= "Zinc finger domain 2"
FT 177..197
FT /note= "Zinc finger domain 3"
FT 384..540
FT /note= "TRAF domain"
PN WO9616665-A1.
PD 06-JUN-1996.
PF 04-DEC-1995; U15695.

PR 02-DEC-1994; US-349357.
PA (LJOL-) LA JOLIA CANCER RES FOUND.
PI Reed JC, Sato T;
DR WPT: 96-286818/29.
DR N-PSDB: T30773.
PT New CD40 associated protein, agonists and antagonists - used to
PT modulate cell proliferation, immune response, apoptosis etc., e.g.
PT for treating cancer or autoimmune disease
PS Claim 3, Fig 1: 94pp: English.
CC This is a CD40 associated protein (CAP)-1. This CAP is a protein that
CC specifically binds to CD40, a cell surface receptor involved in
CC apoptosis. Agonists and antagonists of CAP can increase or decrease
CC the level of CAP expression in a cell and can thereby modulate the
CC function of the cell. Such compounds can be used to treat cancer,
CC autoimmune diseases like asthma, hay fever, rheumatoid arthritis and
CC immunodeficiency diseases and neurodegeneration. Antibodies that bind
CC specifically to CAP can be used to assay CAP, to detect pathologically
CC altered genes. The encoding nucleic acid can be used to identify
CC related genes and to express CAP for gene therapy.
SQ Sequence 543 AA;

Query Match 93.3%; Score 2804; DB 1; Length 543;
Best Local Similarity 94.7%; Pred. No. 6.6e-213;
Matches 538; Conservative 0; Mismatches 4; Indels 26; Gaps 2;

QY 1 MESSKMDSPGALQTNPKLHTDSAGTPVPPGQGGKEKFKVTEDEKCEKCHLV 60
DB 1 MESSKMDSPGALQTNPKLHTDSAGTPVPPGQGGKEKFKVTEDEKCEKCHLV 60
QY 61 CSPKQTECHRCESCMALLSSSPKCTACQESTYKDVFNCKCKREILAQIYCRNE 120
DB 61 CSPKQTECHRCESCMALLSSSPKCTACQESTYKDVFNCKCKREILAQIYCRNE 120
QY 121 SSGCAEQMLG-HLVHAKNDCHFEELPCVRPDCKEKYLKRDLDHYEKACKYREATCSHC 179
DB 121 SSGCAEQMLG-HLVHAKNDCHFEELPCVRPDCKEKYLKRDLDHYEKACKYREATCSHC 180
QY 180 KSOVPMIALQKHEDTDCPCVVVSCPHKCSVQTLNSELSAHLSECVNAPSTCSFKRYGCV 239
DB 181 KSOVPMIALQKHEDTDCPCVVVSCPHKCSVQTLNSELSAHLSECVNAPSTCSFKRYGCV 217
QY 240 FQGTNOQIAHASSAVQVHNLKEMNSLEKVSILLQNESVEKNSISLHNOICSEFI 299
DB 218 --GTNNOIAHASSAVQVHNLKEMNSLEKVSILLQNESVEKNSISLHNOICSEFI 275
QY 300 EIEROKEMLRNNEKSLHLOVYIDSOAEKLEKELKEIRPFQRMWEADSKSSVESLQNR 359
DB 276 EIEROKEMLRNNEKSLHLOVYIDSOAEKLEKELKEIRPFQRMWEADSKSSVESLQNR 335
QY 360 VTELESVDKSAGOVARNITGLLESQSLSRHDQMLSVHDIRLADMDLGFQVLETASYNGVLIM 419
DB 336 VTELESVDKSAGOVARNITGLLESQSLSRHDQMLSVHDIRLADMDLGFQVLETASYNGVLIM 395
QY 420 KIRDYRRKROEAVMGKTLISYQPFYTGFGYKMCARVYLNDGMRGTHLSLFEVIMRG 479
DB 396 KIRDYRRKROEAVMGKTLISYQPFYTGFGYKMCARVYLNDGMRGTHLSLFEVIMRG 455
QY 480 EYDALLPMPFKOKVITLMDQSSRRHLGDARFDPNNSSEFFKPTGEMNIAAGCPVFAVQ 539
DB 456 EYDALLPMPFKOKVITLMDQSSRRHLGDARFDPNNSSEFFKPTGEMNIAAGCPVFAVQ 515
QY 540 TVLENGTYIKDITFIKVIYDTSDDLDP 567
DB 516 TVLENGTYIKDITFIKVIYDTSDDLDP 543

RESULT 8
W27436
ID W27436 standard; Protein: 516 AA.
AC W27436;
DE 27-MAR-1998 (first entry)
Human CRAFL-b isoform p70del8.9.

KM CD40 receptor associated factor 1; CRAF1-b; TRAF-3; p70; human;
 KM CD40 mediated intracellular signalling; organ rejection; allergy;
 KM hay fever; autoimmune disease; systemic lupus erythematosus;
 KM rheumatoid arthritis; myasthenia gravis; Graves' disease;
 KM idiopathic thrombocytopenia purpura; haemolytic anaemia;
 KM diabetes mellitus; psoriasis; hyper immunoglobulin E syndrome;
 KM apoptosis; Riecher's syndrome; spondyloarthritis; Lyme disease; HIV;
 KM syphilis; tuberculosis; arthritis; scleroderma; pulmonary fibrosis;
 KM pneumoconiosis; adult respiratory distress syndrome; pneumonitis;
 KM asbestosis; silicosis; Farmer's lung; hepatitis; cirrhosis;
 KM glomerulosclerosis; multiple sclerosis; glomerulonephritis;
 KM glomerulonephritis; kidney disease; nephropathy;
 KM Henoch-Schoenlein purpura; polyarteritis; multiple myeloma;
 KM Wegener's granulomatosis; cryoglobulinemia;
 KM Waldenstrom's macroglobulinemia; amyloidosis; Sjogren's syndrome;
 KM AIDS; oesophageal dysmotility; inflammatory bowel disease;
 KM Burkitt's lymphoma; nasopharyngeal carcinoma; pneumonia;
 KM gene therapy; diagnosis.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Domain 52..122
 FT /label= "CRAF-b, domain
 FT /note= "C1a1m 1"
 FT 239..263
 FT /note= "zinc finger 1 (zn binding to Cys-239,
 FT Cys-246, His-258 and Cys-263)"
 FT Region
 FT /note= "zinc finger 2 (zinc binding to Cys-270,
 FT Cys-275, His-287 and Cys-292)"
 FT Binding_site 16..19
 FT /note= "putative SH3 binding motif"
 FT Binding_site 44..47
 FT /note= "putative SH3 binding motif"
 FT Binding_site 103..110
 FT /note= "putative SH3 binding motif"
 FT MO9734473-A1.
 PD 25-SEP-1997; D05076.
 PE 21-MAR-1997; D05076.
 PR 18-SEP-1996; US-026584.
 PR 21-MAR-1996; US-013820.
 PR 01-MAY-1996; US-016626.
 PR 01-MAY-1996; US-016659.
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 PA Cleary AM, Frank DM, Lederman S;
 WP1: 97-479907/44.
 N-PSDB; T90123.
 PT Protein comprising CRAF1-b domain capable of inhibiting CD40
 PT mediated cell activation - useful to treat conditions characterised
 PT by aberrant or unwanted level of CD40 mediated intracellular
 PT signalling
 PT Example 1; Fig 1A-O; 158bp; English.
 CC This polypeptide comprises a CRAF1 (TRAF-3) protein designated
 CC p70del8.9 that is encoded by exons 1-2, 4-7 and 10-13 of the human
 CC CRAF gene (see T90123). Different isoforms (W27428-37) of CRAF1
 CC have been identified that arise from alternative splicing. CRAF1
 CC peptides comprising from 0-4 zinc finger domains, and nucleic acids
 CC encoding them, can be used to inhibit CD40 ligand activation of
 CC cells that express CD40 on their surface, particularly by
 CC introducing the nucleic acid molecule into the cells, and used to
 CC treat conditions characterised by an aberrant or unwanted level of
 CC CD40 mediated intracellular signalling, such as organ rejection, or
 CC a CD40 dependent immune response in a subject receiving gene
 CC therapy. The condition may be an allergic response or an
 CC autoimmune response, or may be dependent on CD40 ligand-induced
 CC activation of epithelial cells, an inflammatory kidney disease, a
 CC smooth muscle cell-dependent disease, or a condition associated
 CC with Epstein-Barr virus.
 CC Sequence 516 AA.

Query Match

88.3%; Score 2652.5; DB 1; Length 516;

Best Local Similarity 90.3%; Pred. No. 5, 3e-201;
 Matches 513; Conservative 0; Mismatches 2; Indels 53; Gaps 2;
 QY 1 MESSKMDSPGALQTNPLKHTDRSAGTPEVPEOGYKEKEFKVTEDEKCEKCHLV 60
 DB 1 MESSKMDSPGALQTNPLKHTDRSAGTPEVPEOGYKEKEFKVTEDEKCEKCHLV 60
 QY 61 CSKQTECGHGFESCAALLSSSPKCTACQGSYKDKYFKDNCKRETLAQYCRNE 120
 DB 61 CSKQTECGHGFESCAALLSSSPKCTACQGSYKDKYFKDNCKRETLAQYCRNE 120
 QY 121 SRGAEOLMIGH-LYHDKNCHEEELPCVPDCKEKLRELDLHDYKACKYREATCSHC 179
 DB 121 SRGAEOLMIGH-LYHDKNCHEEELPCVPDCKEKLRELDLHDYKACKYREATCSHC 180
 QY 180 KSGVPMIALQKHEDTDCPCVAVSCPHKCSVQTLRSELSAHLSVCVAPSTCSFKRYGCY 239
 DB 181 KSGVPMIALQKHEDTDCPCVAVSCPHKCSVQTLRSELSAHLSVCVAPSTCSFKRYGCY 239
 QY 240 FQGTNOQIRKHEASSAVOHVNLKEMNSLEKRVSLQNSVEKNSIOSLHNOICFET 299
 DB 190 -QGTNOQIRKHEASSAVOHVNLKEMNSLEKRVSLQNSVEKNSIOSLHNOICFET 248
 QY 300 EIRROKEMLNNSKILHLQRVIDSQAEKLEKDEIRPROMWEADSKSSVESIQNR 359
 DB 249 EIRROKEMLNNSKILHLQRVIDSQAEKLEKDEIRPROMWEADSKSSVESIQNR 308
 QY 360 VTELESYDKSAGVARNRTGLLESQLSRHQMLSVHDIRLADMQLGQVLETAASYGVLIW 419
 DB 309 VTELESYDKSAGVARNRTGLLESQLSRHQMLSVHDIRLADMQLGQVLETAASYGVLIW 368
 QY 420 KIRDYRRKQEAVMGKTLSTXSPFTYGYGKCAVYINGMGMGTHLSFVYIMRG 479
 DB 369 KIRDYRRKQEAVMGKTLSTXSPFTYGYGKCAVYINGMGMGTHLSFVYIMRG 428
 QY 480 EYDALLPMPFKQVTLMLMDQSSRRHLGDAFKPDPSSFFKPTGEMNTASGCPVVAO 539
 DB 429 EYDALLPMPFKQVTLMLMDQSSRRHLGDAFKPDPSSFFKPTGEMNTASGCPVVAO 488
 QY 540 TVLENGTYINDTIFIKVIYDTSDDLPDP 567
 DB 489 TVLENGTYINDTIFIKVIYDTSDDLPDP 516
 RESULT 9
 ID W27437
 AC W27437
 DT 27-MAR-1998 (first entry)
 DE Human CRAF1-b isoform p70del8.9
 KW CD40 receptor associated factor 1; CRAF1-b; TRAF-3; p70; human;
 KW CD40 mediated intracellular signalling; organ rejection; allergy;
 KW hay fever; autoimmune disease; systemic lupus erythematosus;
 KW rheumatoid arthritis; myasthenia gravis; Graves' disease;
 KW idiopathic thrombocytopenia purpura; haemolytic anaemia;
 KW diabetes mellitus; psoriasis; hyper immunoglobulin E syndrome;
 KW apoptosis; Riecher's syndrome; spondyloarthritis; Lyme disease; HIV;
 KW syphilis; tuberculosis; arthritis; scleroderma; pulmonary fibrosis;
 KW pneumoconiosis; adult respiratory distress syndrome; pneumonitis;
 KW asbestosis; silicosis; Farmer's lung; hepatitis; cirrhosis;
 KW glomerulosclerosis; multiple sclerosis; glomerulonephritis;
 KW glomerulonephritis; kidney disease; nephropathy;
 KW endocarditis; leprosy; malaria; Goodpasture's disease;
 KW Henoch-Schoenlein purpura; polyarteritis; multiple myeloma;
 KW Wegener's granulomatosis; cryoglobulinemia;
 KW Waldenstrom's macroglobulinemia; amyloidosis; Sjogren's syndrome;
 KW AIDS; oesophageal dysmotility; inflammatory bowel disease;
 KW Burkitt's lymphoma; nasopharyngeal carcinoma; pneumonia;
 KW gene therapy; diagnosis.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Domain 52..122

Sat Sep 2 10:45:20 2000

us-09-224-556-2.raj

FT /label= CRAFT-b domain
FT /note= "Claim 1"
FT 239. .263
FT /note= "zinc finger 1 (Zn binding to Cys-239,
FT Cys-246, His-258 and Cys-263)"
FT Region
FT 270. .292
FT /note= "zinc finger 2 (zinc binding to Cys-270,
FT Cys-275, His-287 and Cys-292)"
FT Binding_site
FT 16. .19
FT /note= "putative SH3 binding motif"
FT Binding_site
FT 44. .47
FT /note= "putative SH3 binding motif"
FT Binding_site
FT 103. .110
FT /note= "putative SH3 binding motif"
FT W09734473-A1.
FT 25-SEP-1997. U05076.
FT 21-MAR-1997. U05076.
FT 18-SEP-1996. US-026584.
FT 21-MAR-1996. US-013820.
FT 01-MAY-1996. US-016626.
FT 01-MAY-1996. US-016659.
FT (UYCO) UNIV COLUMBIA NEW YORK.
FT Cleary AM, Frank DM, Lederman S.
FT WPI: 97-479907/44.
DR N-PSDB: T90123.
PT Protein comprising CRAFT-b domain capable of inhibiting CD40
PT mediated cell activation - useful to treat conditions characterised
PT by aberrant or unwanted level of CD40 mediated intracellular
PT signalling
PT Example 1: Fig 1A-C: 158bp; English.
PT This polypeptide comprises a CRAFT (TRAF-3) protein designated
PT p70123, that is encoded by exons 1-2, 4-7 and 10-13 of the human
PT CRAFT gene (see T90123). Different isoforms (W27428-37) of CRAFT
PT have been identified that arise from alternative splicing. CRAFT
PT peptides comprising from 0-4 zinc finger domains, and nucleic acids
PT encoding them, can be used to inhibit CD40 ligand activation or
PT cells that express CD40 on their surface, particularly by
PT introducing the nucleic acid molecule into the cells, and used to
PT treat conditions characterised by an aberrant or unwanted level of
PT CD40 mediated intracellular signalling, such as organ rejection, or
PT a CD40 dependent immune response in a subject receiving gene
PT therapy. The condition may be an allergic response or an
PT autoimmune response, or may be dependent on CD40 ligand-induced
PT activation of epithelial cells, an inflammatory kidney disease, a
PT smooth muscle cell-dependent disease, or a condition associated
PT with Epstein-Barr virus.
PT Sequence 638 AA;
Query Match 88.3%; Score 2652.5; DB 1; Length 638;
Best Local Similarity 90.3%; Pred. No. 7.1e-201; Indels 53; Gaps 2;
Matches 513; Conservative 0; Mismatches 2;
OY 1 MESSKKMSPGALQTNPLKLTDRSAGTPVPEOGYKEKYEVEDKCKCHLYL 60
DB 123 MESSKKMSPGALQTNPLKLTDRSAGTPVPEOGYKEKYEVEDKCKCHLYL 182
OY 61 CSFKOTEGCHRCESCMALLSSSPKCTACQESTIVDKYKNDCKCKREILALQYCRNE 120
DB 183 CSFKOTEGCHRCESCMALLSSSPKCTACQESTIVDKYKNDCKCKREILALQYCRNE 242
OY 121 SRGAEQMLGR-LVHLKNDCHFEELPCVRPCKEKLKDLRDHVEKAKYREATCSHC 179
DB 243 SRGAEQMLGR-LVHLKNDCHFEELPCVRPCKEKLKDLRDHVEKAKYREATCSHC 302
OY 180 KSOVPMALQKHEDTDCPVVSCPHKCSVOLLNSELNLSPECVNAPTCSFRKYGCV 239
DB 303 KSOVPMALQKHEDTDCPVVSCPHKCSVOLLNSELNLSPECVNAPTCSFRKYGCV 311
OY 240 FOGTNOQIKAHASAVOHNVLKEMSNLEKYSLLQNSYKNSIOSLHNOJCSFEI 299
DB 312 -OGTNOQIKAHASAVOHNVLKEMSNLEKYSLLQNSYKNSIOSLHNOJCSFEI 370

OY 300 EIEROKEMLRNNEKILHLOVIDSOAEKLEKDEIRPFROMWEADSMKSSVESLONR 359
DB 371 EIEROKEMLRNNEKILHLOVIDSOAEKLEKDEIRPFROMWEADSMKSSVESLONR 430
OY 360 VTELESVDKSAQAVANTGLLESQSLSRHDOMLSYHDIRLADMDLGFQVLETASYNGVLM 419
DB 431 VTELESVDKSAQAVANTGLLESQSLSRHDOMLSYHDIRLADMDLGFQVLETASYNGVLM 490
OY 420 KIRDIYKROEAMVGTSLSYQPFYTGFGKMCARVYLNGDMGKSTLSFEVIMRG 479
DB 491 KIRDIYKROEAMVGTSLSYQPFYTGFGKMCARVYLNGDMGKSTLSFEVIMRG 550
OY 480 EYDALPWPPEKQVLTMLMDQSSRHGDAKPPDNSSFFKPTGEMNITASGCPVVAQ 539
DB 551 EYDALPWPPEKQVLTMLMDQSSRHGDAKPPDNSSFFKPTGEMNITASGCPVVAQ 610
OY 540 TVLENGITINDTIFIKVIVDTSLDLP 567
DB 611 TVLENGITINDTIFIKVIVDTSLDLP 638
RESULT 10
W27434
W27434 standard; Protein: 512 AA.
ID W27434:
AC 27-MAR-1998 (first entry)
DE Human CRAFT isoform p55del9.10.
KW CD40 receptor associated factor 1; CRAFT-a; TRAF-3; p55; human;
KW CD40 mediated intracellular signalling; organ rejection; allergy;
KW hay fever; autoimmune disease; systemic erythematosis;
KW rheumatoid arthritis; myasthenia gravis; Graves' disease;
KW idiopathic thrombocytopenia purpura; haemolytic anaemia;
KW diabetos mellitus; psoriasis; hyper immunoglobulin E syndrome;
KW apoptosis; Rieger's syndrome; spondylarthritis; Lyme disease; HIV;
KW syphilis; tuberculosis; adult respiratory distress syndrome; pneumonitis;
KW pneumoconiosis; Farmer's lung; hepatitis; cirrhosis;
KW glomerulosclerosis; multiple sclerosis; kidney disease; nephropathy;
KW atherosclerosis; glomerulopathy; Goodpasture's disease;
KW endocarditis; leprosy; malaria; polyarteritis; multiple myeloma;
KW Henoch-Schoenlein purpura; polyarteritis; multiple myeloma;
KW Wegener's granulomatosis; cryoglobulinemia; amyloidosis; Sjogren's syndrome;
KW Waldenstrom's macroglobulinemia; amyloidosis; Sjogren's syndrome;
KW AIDS; oesophageal dysmotility; inflammatory bowel disease;
KW bladder disease; Epstein-Barr virus; mononucleosis; B cell tumour;
KW Burkitt's lymphoma; nasopharyngeal carcinoma; pneumonia;
KW gene therapy; diagnosis.
OS Homo sapiens.
FH Key
FT Region Location/Qualifiers
FT 117. .141
FT /note= "zinc finger 1 (Zn binding to Cys-117,
FT Cys-124, His-136 and Cys-141)"
FT Region
FT 148. .170
FT /note= "zinc finger 2 (zinc binding to Cys-148,
FT Cys-153, His-165 and Cys-170)"
FT Region
FT 177. .197
FT /note= "zinc finger 3 (Zn binding to Cys-177,
FT Cys-180, His-192 and Cys-197)"
FT W09734473-A1.
FT 25-SEP-1997. U05076.
FT 21-MAR-1997. U05076.
FT 18-SEP-1996. US-026584.
FT 21-MAR-1996. US-013820.
FT 01-MAY-1996. US-016626.
FT 01-MAY-1996. US-016659.
FT (UYCO) UNIV COLUMBIA NEW YORK.
FT Cleary AM, Frank DM, Lederman S.
FT WPI: 97-479907/44.
DR N-PSDB: T90123.
PT Protein comprising CRAFT-b domain capable of inhibiting CD40
PT mediated cell activation - useful to treat conditions characterised
PT by aberrant or unwanted level of CD40 mediated intracellular
PT signalling

CC activation of epithelial cells, an inflammatory kidney disease, a
CC smooth muscle cell-dependent disease, or a condition associated
CC with Epstein-Barr virus.
50 Sequence 634 AA;

Query Match	88.18;	Score 2646.5;	DB 1;	length 634;
Best Local Similarity	89.68;	Pred. No. 2.1e-200;		
Matches 509; Conservative	0;	Mismatches 2;	Indels 57;	Gaps 2.

QY 1 MESSKRMDSFGALDINPLPLKATHTRSAGTIVPEVDEGGYKEKVKVIEEDKFKCKCHLV 60

Db 123 MESSKRMDSFGALDINPLPLKATHTRSAGTIVPEVDEGGYKEKVKVIEEDKFKCKCHLV 182

QY 61 CSPKOTEGGHFCSCHMAALLSSSSPKCTAQOESIYVDKFKPNCKKRETLAQITCRNE 120

Db 183 CSPKOTEGGHFCSCHMAALLSSSSPKCTAQOESIYVDKFKPNCKKRETLAQITCRNE 242

QY 121 SRGCEQLOALMTH-LVHLKNDCHFELPCVRPDCCKEYLRKDLNDHYEKACKYREATCSHC 179

Db 243 SRGCEQLOALMTH-LVHLKNDCHFELPCVRPDCCKEYLRKDLNDHYEKACKYREATCSHC 302

QY 180 KSQVPMIALQKHEDTDCVYVSCSPHKCSVQTLTLRSELSAHLSBCVNAFSTCSFKRYGCY 239

Db 303 KSQVPMIALQKHEDTDCVYVSCSPHKCSVQTLTLRSELSAHLSBCVNAFSTCSFKRYGCY 339

QY 240 FQGTNQIKAHASSAVOHVNLKEMSNSEKRVSLLOÑESVEKKNKSIOGLHNOICFEL 299

Db 340 -----VSLLOÑESVEKKNKSIOGLHNOICFEL 366

QY 300 EIERKEKMLRNNESSITLHLORVIDISOAEKLEKDEKREIPRONMEEADSKSSVESLQNR 359

Db 367 EIERKEKMLRNNESSITLHLORVIDISOAEKLEKDEKREIPRONMEEADSKSSVESLQNR 426

QY 360 VTELESYDKSAGQVARNRTGTLLESOLSRHDQMLSYHDRIADMDLGFOVLETASVNGVLIW 419

Db 427 VTELESYDKSAGQVARNRTGTLLESOLSRHDQMLSYHDRIADMDLRQVLETASVNGVLIW 486

QY 420 KIRDYKRRRKOBAVNGKTLISYQPFYTGFGYKMKCARVYINGDGMKGTHLSLFVYIMRG 479

Db 467 KIRDYKRRRKOBAVNGKTLISYQPFYTGFGYKMKCARVYINGDGMKGTHLSLFVYIMRG 546

QY 480 EYDALLPMPFQOKYTLMLMDGSSRRHLGDAFKRDPNMSSEFKRPTGEMNTASGCPYFVAQ 539

Db 547 EYDALLPMPFQOKYTLMLMDGSSRRHLGDAFKRDPNMSSEFKRPTGEMNTASGCPYFVAQ 606

QY 540 TYLENGTYIKDDTIFIKYIVDTSLPDP 567

Db 607 TYLENGTYIKDDTIFIKYIVDTSLPDP 634

RESULT 12

R88835

ID R88835 standard; Protein; 472 AA.

AC R88835;

DT 23-MAR-1998 (first entry)

DE CD40 associated protein (CAP)-1 clone pSK-7 (residues 82-543).

KW CD40 associated protein; CAP; agonist; antagonist; gene therapy; cell proliferation; treatment; cancer; autoimmune disease.

OS Homo sapiens.

PN W0961665-A1.

PD 06-JUN-1996.

PF 04-DEC-1995; U15695.

PR 02-DEC-1994; U5-349357.

PA (LJOL-) LA JOLIA CANCER RES FOUND.

PI Reed JC, Sato T;

WP: 96-286818/29.

PT New CD40 associated protein, agonists and antagonists - used to modulate cell proliferation, immune response, apoptosis etc., e.g. for treating cancer or autoimmune disease

PS Claim 5; Page -: 94pp; English.

CC This is a clone of the CD40 associated protein (CAP)-1. This clone pSK-7 encodes amino acids 82 to 543 of CAP-1. The CAP specifically binds

CC to CD44 cell surface receptor involved in apoptosis. Agonists and
CC antagonists of CAP can increase or decrease the level of CAP expression
CC in a cell and can thereby modulate the function of the cell. Such
CC compounds can be used to treat cancer, autoimmune diseases like asthma,
CC hay fever, rheumatoid arthritis and immunodeficiency diseases and
CC neurodegeneration. Antibodies that bind specifically to CAP can be used
CC to assay CAP, to detect pathologically altered levels. The CAP-1 encoding
CC nucleic acid can be used to identify related genes and to express CAP
CC for gene therapy.
CC Note: This sequence does not appear in the specification. It has
CC been created from the parent CAP-1 sequence provided in Fig 1.
SQ Sequence 472 AA;

Query Match	Similarity	80.4%	Score 2416	DB 1	Length 472
Best Local	Similarity	94.2%	Pred. No. 2e-182		
Matches	467	Conservative	0	Mismatches	3
				Indels	26
				Gaps	2
QY	73	CESCAALSSSSPCTCAQESIVADKYFKDCCREIILAIQYCRNBSRGCAEOLMTGH	132		
Db	2	CESCAALSSSSPCTCAQESIVADKYFKDCCREIILAIQYCRNBSRGCAEOLMTGH	61		
QY	133	LVHLKNDCHFEELCYVRPDCKEKYLKRDLDHVEKACKYREATCSHCKSQVPMIALKH	191		
Db	62	LVHLKNDCHFEELCYVRPDCKEKYLKRDLDHVEKACKYREATCSHCKSQVPMIALKH	121		
QY	192	EDTDCPCVAVSCPHKCSVOTILRLSELSAHLSECVNAPSTCSFKRYGCVFOGTNOQIKAE	251		
Db	122	EDTDCPCVAVSCPHKCSVOTILRLSEL-----GTNOQIKAE	156		
QY	252	ASSAVOHNVLKEMNSLEKAYSLIQNSVEKNSIOSLIHNOICSEFIEIEKREMLRNN	311		
Db	157	ASSAVOHNVLKEMNSLEKAYSLIQNSVEKNSIOSLIHNOICSEFIEIEKREMLRNN	216		
QY	312	ESKILHLQHVIDSQAELKELDKEIRPEPRONNEEADSMKSSVESIQNRYTELESYDKSAG	371		
Db	217	ESKILHLQHVIDSQAELKELDKEIRPEPRONNEEADSMKSSVESIQNRYTELESYDKSAG	276		
QY	372	QVARNLTGILLSRLSDQLSVHDIRLADMDLGFOVLELASYNGVLIWKIRDYKRRKOA	431		
Db	277	QVARNLTGILLSRLSDQLSVHDIRLADMDLRFVLELASYNGVLIWKIRDYKRRKOA	336		
QY	432	VNGKLTSLTSGPEFYGYEYKMKCAVYIANGCMGKGTSLSEFYVIMRGDYDLLPMPFO	491		
Db	337	VNGKLTSLTSGPEFYGYEYKMKCAVYIANGCMGKGTSLSEFYVIMRGDYDLLPMPFO	396		
QY	492	KYTLIMDMOGSSRRHLGDAFKPDPNSSSEFKRTGEMINLASGCPVAVQTVLENGYTIKDD	551		
Db	397	KYTLIMDMOGSSRRHLGDAFKPDPNSSSEFKRTGEMINLASGCPVAVQTVLENGYTIKDD	456		
QY	552	TIFIKYIVYDSDLDPD	567		
Db	457	TIFIKYIVYDSDLDPD	472		
RESULT	13				
ID	W29257				
AC	W29257	standard; Protein: 558 AA.			
DE	18-MAR-1998	(first entry)			
DE	Murine TRAF5, a novel TNF receptor associated factor family protein.				
KW	TRAF5; tumour necrosis factor receptor; TNF;				
OS	Murine sp.				
PN	MO9731110-AL				
PD	28-AUG-1997				
PF	24-FEB-1997	J00512.			
PR	22-FEB-1996	JP-034674.			
PA	(SUME) SUMITOMO ELECTRIC IND CO.				
PI	Nakano H, Nakata M, Okumura K, Yagita H;				
DR	WPI: 97-435162/40.				
DR	N-PSDB; T87039				
PT	Tumour necrosis factor receptor associated factor family protein,				

PD 28-AUG-1997. J00512.
PR 24-FEB-1997. J00512.
PR 22-FEB-1996. JP-034674.
PA (SUME) SUMITOMO ELECTRIC IND CO.
PI Nakano H, Nakata M, Okumura K, Yagita H;
WPI: 97-435162/40.
DR N-PSDB: T87040.
DR Tumor necrosis factor receptor associated factor family protein,
PT TRAF5 - useful to study signal transduction in tumour necrosis
PT factor receptor family
PS Claim 3: Pages 46-49, 69pp. Japanese.
CC The present sequence represents a novel protein, designated TRAF5, which
CC is a member of the tumour necrosis factor (TNF) receptor associated
CC factor family. The TRAF5 protein has a coiled-coil domain, a leucine
CC zipper motif and binds to lymphotoxin beta receptor and to CD30, but not
CC to CD40 or TNF receptor 2. TRAF5 and its corresponding DNA are useful for
CC the investigation of the signal transducer system of the TNF receptor
CC family and the functions of TRAF proteins. They can also be used as
CC probes for research and diagnostic purposes, and investigation of the
CC specific applications of potential therapeutic agents.
SO Sequence 557 AA;

Query Match 39.3%; Score 1182; DB 1; Length 557;
Best Local Similarity 41.6%; Pred. No. 3.8e-85;
Matches 229; Conservative 121; Mismatches 181; Indels 20; Gaps 8;

QY 25 RSAGTPEVPEOGGKREKRYKVEKDYEDKCKEHLVLCSPKOTEGHRCFSCMAALLS-S 83
DB 17 QNSGNSISIDFEPSEIEYOFVERLEERKCAFCVSHNHQTCGHRFCOHCILSREIN 76
QY 84 SSPKCTAOESIVADKYKNDKCKREILAIQYCRNESRCABOLMGLVHLKNDCHRE 143
DB 77 TVPICVDKREIKSOEYKNDCKREVLNLYVCSN-APGNAKVIIGRYODHLQOCLFQ 135
QY 144 ELPCVPRPCKREKRLKDIIDHVEKAKYREATCSHCQVPMALOKHEPTDCPCVAVSC 203
DB 136 PVQGENCKREVLKRLKELSLASQCFRKEKCLYCKKDVVIMLQNHENLCEYDVFPC 195
QY 204 PHKCSVOTLLRELSAHLSECVNAPSTCSFRKYGCVFQGTNOQIKAHBASAVOHVNLK 263
DB 196 FNNCA-KIILKEVEHDLAVCPAEQDCPFHYGCAVTDKRRNLQOEHSHALREHMLVL 254
QY 264 EMSNSLEKRVSLQNESVEKNSIOSLNQJCSPEIEIEKOKEMLRNNESKILHLQVID 323
DB 255 EKNVQLEEQISDLHKSLEQKESKIQOLAEITIKLEKEKQPAQLFGKNGSLPNIQ-VFA 313
QY 324 SQAERIKELDKELRPF-----RONWEADSMKSSVESLQNRVTELESVDKSAGQVANT 377
DB 314 SHIDKSAMLEAOVHQLQAVNOQKFDLRPLMEAVDVTYKOKITLLENND-----QRL 366
QY 378 GILESQLSRHQMLVSHDIRLADMDIGFOVLETASYNGVLYIKIRYKRRKQEAVMGKTL 437
DB 367 AVLEEFENKHDTHINIHKAQLSKNEREFKLGCTGYNGLIMKYDYKKKREAVDGHIV 426
QY 438 SLXSQPFYGYGFKKACARYLNGDGMGKTHLSLFVIMRGEYDALLPMPKQKRVTLML 497
DB 427 SIFSQSYTSCGRLCARAYLNGDGSRGSHLSLFVVMRGFDSLLQMPFRQRYTLML 486
QY 498 MDQSSRRHLGDAFKPDPNSSSKKPTGEMNINASGCPVFAQTVLEN--GYIKDDTIFI 555
DB 487 LDQ-SGKKNIEMTFKPPDNSSSKKRPDGENNINASGCPFAHSAVLNANAYIKDDTIFL 545
QY 556 KVIYDTSDDLP 566
DB 546 KVAVDLTDLDD 556